SEQUENCE LISTING

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Jenkins, Yonchu
Markovtsov, Vadim
Rigel Pharmaceuticals, Inc.

<120> Modulators of Cellular Proliferation

<130> 021044-004010US

<140> US 10/620,052
<141> 2003-07-14

<150> US 60/395,443
<151> 2002-07-12

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<170> PatentIn Ver. 2.1

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Pro Lys Asp Pro Lys Leu Arg Glu Leu Leu Asp Val Gly Asn Ile Gly
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Lys Thr Ser Pro Phe Pro Ile Leu Leu Ser Phe Glu Asn His Val Asp
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<210> 6
<211> 879
<212> PRT
<213> Homo sapiens

<220>
<223> cytoplasmic tyrosine kinase focal adhesion kinase
(FAK)

<400> 6
Met Ser Asp Tyr Trp Val Val Gly Lys Lys Ser Asn Tyr Glu Val Leu
1 5 10 15

Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro Lys Ser Leu Leu Asp
20 25 30

Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile Gln Gln Thr Phe Arg
35 40 45

Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile Leu Lys Phe Phe Glu
50 55 60

Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys Phe Lys Cys Ala
65 70 75 80

Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu Ala Ile Gly Pro Glu
85 90 95

Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn Pro Thr His Leu
100 105 110

Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr Ser Asn Ser Glu Asp
115 120 125

Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala Gly Ala Pro Glu
130 135 140

```
Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile Ala Glu Asn Met Ala
145                 150                 155                 160

Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn Gly Thr Ser Gln Ser
                165                 170                 175

Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg Ala Leu Pro Ser Ile
            180                 185                 190

Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met Arg Thr His Ala Val
        195                 200                 205

Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile Ile Asp Glu Glu Asp
    210                 215                 220

Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu Ile Gln Arg Glu Arg
225                 230                 235                 240

Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln Phe Gly Asp Val His
                245                 250                 255

Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala Leu Ala Val Ala Ile
            260                 265                 270

Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val Arg Glu Lys Phe Leu
        275                 280                 285

Gln Glu Ala Cys His Tyr Thr Ser Leu His Trp Asn Trp Cys Arg Tyr
    290                 295                 300

Ile Ser Asp Pro Asn Val Asp Ala Cys Pro Asp Pro Arg Asn Ala Glu
305                 310                 315                 320

Leu Thr Met Arg Gln Phe Asp His Pro His Ile Val Lys Leu Ile Gly
                325                 330                 335

Val Ile Thr Glu Asn Pro Val Trp Ile Ile Met Glu Leu Cys Thr Leu
            340                 345                 350

Gly Glu Leu Arg Ser Phe Leu Gln Val Arg Lys Tyr Ser Leu Asp Leu
        355                 360                 365

Ala Ser Leu Ile Leu Tyr Ala Tyr Gln Leu Ser Thr Ala Leu Ala Tyr
    370                 375                 380

Leu Glu Ser Lys Arg Phe Val His Arg Asp Ile Ala Ala Arg Asn Val
385                 390                 395                 400

Leu Val Ser Ser Asn Asp Cys Val Lys Leu Gly Asp Phe Gly Leu Ser
                405                 410                 415

Arg Tyr Met Glu Asp Ser Thr Tyr Tyr Lys Ala Ser Lys Gly Lys Leu
            420                 425                 430

Pro Ile Lys Trp Met Ala Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr
        435                 440                 445

Ser Ala Ser Asp Val Trp Met Phe Gly Val Cys Met Trp Glu Ile Leu
    450                 455                 460
```

```
Met His Gly Val Lys Pro Phe Gln Gly Val Lys Asn Asn Asp Val Ile
465                 470                 475                 480

Gly Arg Ile Glu Asn Gly Glu Arg Leu Pro Met Pro Pro Asn Cys Pro
                485                 490                 495

Pro Thr Leu Tyr Ser Leu Met Thr Lys Cys Trp Ala Tyr Asp Pro Ser
            500                 505                 510

Arg Arg Pro Arg Phe Thr Glu Leu Lys Ala Gln Leu Ser Thr Ile Leu
        515                 520                 525

Glu Glu Glu Lys Ala Gln Gln Glu Glu Arg Met Arg Met Glu Ser Arg
    530                 535                 540

Arg Gln Ala Thr Val Ser Trp Asp Ser Gly Gly Ser Asp Glu Ala Pro
545                 550                 555                 560

Pro Lys Pro Ser Arg Pro Gly Tyr Pro Ser Pro Arg Ser Ser Glu Gly
                565                 570                 575

Phe Tyr Pro Ser Pro Gln His Met Val Gln Thr Asn His Tyr Gln Val
            580                 585                 590

Ser Gly Tyr Pro Gly Ser His Gly Ile Thr Ala Met Ala Gly Ser Ile
        595                 600                 605

Tyr Pro Gly Gln Ala Ser Leu Leu Asp Gln Thr Asp Ser Trp Asn His
    610                 615                 620

Arg Ser Gln Glu Ile Ala Met Trp Gln Pro Asn Val Glu Asp Ser Thr
625                 630                 635                 640

Val Leu Asp Leu Arg Gly Ile Gly Gln Val Leu Pro Thr His Leu Met
                645                 650                 655

Glu Glu Arg Leu Ile Arg Gln Gln Gln Glu Met Glu Glu Asp Gln Arg
            660                 665                 670

Trp Leu Glu Lys Glu Glu Arg Phe Leu Ile Gly Asn Gln His Ile Tyr
        675                 680                 685

Gln Pro Val Gly Lys Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro
    690                 695                 700

Arg Pro Gly Ala Pro Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser
705                 710                 715                 720

Pro Ala Asp Ser Tyr Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile
                725                 730                 735

Ser Pro Pro Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr
            740                 745                 750

Glu Asn Val Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys
        755                 760                 765

Ile Gln Pro Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val
    770                 775                 780
```

```
Gly Leu Ala Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro
785                 790                 795                 800

Leu Leu Pro Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu
                805                 810                 815

Leu Asn Ser Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln
            820                 825                 830

Gln Tyr Val Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu
        835                 840                 845

Thr Ala Ala His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val
    850                 855                 860

Ile Asp Gln Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His
865                 870                 875
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<210> 7
<211> 4089
<212> DNA
<213> Homo sapiens

<220>
<223> calcium dependent tyrosine kinase focal adhesion
kinase 2 (FAK2)

<400> 7
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cgctggagtc cgcgcctccc tgggactgca atgtgccgat cttagctgct gcctgagagg 180
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ctgcacgtgg aagccgagtg gaggtatgac cttcaaatcc gctacttgcc agaagacttc 600
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<210> 8
<211> 1009
<212> PRT
<213> Homo sapiens

<220>
<223> calcium dependent tyrosine kinase focal adhesion
kinase 2 (FAK2)

<400> 8

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Met Ser Gly Val Ser Glu Pro Leu Ser Arg Val Lys Leu Gly Thr Leu
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Arg Arg Pro Glu Gly Pro Ala Glu Pro Met Val Val Val Pro Val Asp
            20                  25                  30

Val Glu Lys Glu Asp Val Arg Ile Leu Lys Val Cys Phe Tyr Ser Asn
        35                  40                  45

Ser Phe Asn Pro Gly Lys Asn Phe Lys Leu Val Lys Cys Thr Val Gln
    50                  55                  60
```

```
Thr Glu Ile Arg Glu Ile Ile Thr Ser Ile Leu Leu Ser Gly Arg Ile
 65                  70                  75                  80

Gly Pro Asn Ile Arg Leu Ala Glu Cys Tyr Gly Leu Arg Leu Lys His
                85                  90                  95

Met Lys Ser Asp Glu Ile His Trp Leu His Pro Gln Met Thr Val Gly
            100                 105                 110

Glu Val Gln Asp Lys Tyr Glu Cys Leu His Val Glu Ala Glu Trp Arg
        115                 120                 125

Tyr Asp Leu Gln Ile Arg Tyr Leu Pro Glu Asp Phe Met Glu Ser Leu
    130                 135                 140

Lys Glu Asp Arg Thr Thr Leu Leu Tyr Phe Tyr Gln Gln Leu Arg Asn
145                 150                 155                 160

Asp Tyr Met Gln Arg Tyr Ala Ser Lys Val Ser Glu Gly Met Ala Leu
                165                 170                 175

Gln Leu Gly Cys Leu Glu Leu Arg Arg Phe Phe Lys Asp Met Pro His
            180                 185                 190

Asn Ala Leu Asp Lys Lys Ser Asn Phe Glu Leu Leu Glu Lys Glu Val
        195                 200                 205

Gly Leu Asp Leu Phe Phe Pro Lys Gln Met Gln Glu Asn Leu Lys Pro
    210                 215                 220

Lys Gln Phe Arg Lys Met Ile Gln Gln Thr Phe Gln Gln Tyr Ala Ser
225                 230                 235                 240

Leu Arg Glu Glu Glu Cys Val Met Lys Phe Phe Asn Thr Leu Ala Gly
                245                 250                 255

Phe Ala Asn Ile Asp Gln Glu Thr Tyr Arg Cys Glu Leu Ile Gln Gly
            260                 265                 270

Trp Asn Ile Thr Val Asp Leu Val Ile Gly Pro Lys Gly Ile Arg Gln
        275                 280                 285

Leu Thr Ser Gln Asp Ala Lys Pro Thr Cys Leu Ala Glu Phe Lys Gln
    290                 295                 300

Ile Arg Ser Ile Arg Cys Leu Pro Leu Glu Glu Gly Gln Ala Val Leu
305                 310                 315                 320

Gln Leu Gly Ile Glu Gly Ala Pro Gln Ala Leu Ser Ile Lys Thr Ser
                325                 330                 335

Ser Leu Ala Glu Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys
            340                 345                 350

Arg Leu Gln Gly Glu His Gln Gly Ser Leu Ile Ile His Pro Arg Lys
        355                 360                 365

Asp Gly Glu Lys Arg Asn Ser Leu Pro Gln Ile Pro Met Leu Asn Leu
    370                 375                 380
```

```
Glu Ala Arg Arg Ser His Leu Ser Glu Ser Cys Ser Ile Glu Ser Asp
385                 390                 395                 400

Ile Tyr Ala Glu Ile Pro Asp Glu Thr Leu Arg Arg Pro Gly Gly Pro
                405                 410                 415

Gln Tyr Gly Ile Ala Arg Glu Asp Val Val Leu Asn Arg Ile Leu Gly
            420                 425                 430

Glu Gly Phe Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn His Lys
        435                 440                 445

Gly Glu Lys Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp Cys Thr
    450                 455                 460

Leu Asp Asn Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met Lys Asn
465                 470                 475                 480

Leu Asp His Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu Glu Glu
                485                 490                 495

Pro Thr Trp Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu Gly His
            500                 505                 510

Tyr Leu Glu Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu Val Leu
        515                 520                 525

Tyr Ser Leu Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser Ile Asn
    530                 535                 540

Cys Val His Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala Ser Pro
545                 550                 555                 560

Glu Cys Val Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile Glu Asp
                565                 570                 575

Glu Asp Tyr Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys Trp Met
            580                 585                 590

Ser Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser Asp Val
        595                 600                 605

Trp Met Phe Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly Lys Gln
    610                 615                 620

Pro Phe Phe Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu Glu Lys
625                 630                 635                 640

Gly Asp Arg Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu Tyr Thr
                645                 650                 655

Leu Met Thr Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro Arg Phe
            660                 665                 670

Thr Glu Leu Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu Lys Asp
        675                 680                 685

Ile Ala Met Glu Gln Glu Arg Asn Ala Arg Tyr Arg Thr Pro Lys Ile
    690                 695                 700
```

```
Leu Glu Pro Thr Ala Phe Gln Glu Pro Pro Pro Lys Pro Ser Arg Pro
705                 710                 715                 720

Lys Tyr Arg Pro Pro Pro Gln Thr Asn Leu Leu Ala Pro Lys Leu Gln
                725                 730                 735

Phe Gln Val Pro Glu Gly Leu Cys Ala Ser Ser Pro Thr Leu Thr Ser
            740                 745                 750

Pro Met Glu Tyr Pro Ser Pro Val Asn Ser Leu His Thr Pro Pro Leu
        755                 760                 765

His Arg His Asn Val Phe Lys Arg His Ser Met Arg Glu Glu Asp Phe
    770                 775                 780

Ile Gln Pro Ser Ser Arg Glu Glu Ala Gln Gln Leu Trp Glu Ala Glu
785                 790                 795                 800

Lys Val Lys Met Arg Gln Ile Leu Asp Lys Gln Gln Lys Gln Met Val
                805                 810                 815

Glu Asp Tyr Gln Trp Leu Arg Gln Glu Glu Lys Ser Leu Asp Pro Met
            820                 825                 830

Val Tyr Met Asn Asp Lys Ser Pro Leu Thr Pro Glu Lys Glu Val Gly
        835                 840                 845

Tyr Leu Glu Phe Thr Gly Pro Pro Gln Lys Pro Pro Arg Leu Gly Ala
    850                 855                 860

Gln Ser Ile Gln Pro Thr Ala Asn Leu Asp Arg Thr Asp Asp Leu Val
865                 870                 875                 880

Tyr Leu Asn Val Met Glu Leu Val Arg Ala Val Leu Glu Leu Lys Asn
                885                 890                 895

Glu Leu Cys Gln Leu Pro Pro Glu Gly Tyr Val Val Val Val Lys Asn
            900                 905                 910

Val Gly Leu Thr Leu Arg Lys Leu Ile Gly Ser Val Asp Asp Leu Leu
        915                 920                 925

Pro Ser Leu Pro Ser Ser Ser Arg Thr Glu Ile Glu Gly Thr Gln Lys
    930                 935                 940

Leu Leu Asn Lys Asp Leu Ala Glu Leu Ile Asn Lys Met Arg Leu Ala
945                 950                 955                 960

Gln Gln Asn Ala Val Thr Ser Leu Ser Glu Glu Cys Lys Arg Gln Met
                965                 970                 975

Leu Thr Ala Ser His Thr Leu Ala Val Asp Ala Lys Asn Leu Leu Asp
            980                 985                 990

Ala Val Asp Gln Ala Lys Val Leu Ala Asn Leu Ala His Pro Pro Ala
        995                1000                1005

Glu
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<210> 9
<211> 2195
<212> DNA
<213> Homo sapiens

<220>
<223> serine threonine protein kinase casein kinase 2,
alpha 1 subunit isoform a, transcript variant 2
(CK2, CK2alpha), CK2 catalytic subunit alpha

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(CK2, CK2alpha), CK2 catalytic subunit alpha

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Thr His Arg Pro Arg Glu Tyr Trp Asp Tyr Glu Ser His Val Val Glu
             20                  25                  30

Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly
         35                  40                  45

Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys
     50                  55                  60

Val Val Val Lys Ile Leu Lys Pro Val Lys Lys Lys Ile Lys Arg
 65                  70                  75                  80

Glu Ile Lys Ile Leu Glu Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr
                 85                  90                  95

Leu Ala Asp Ile Val Lys Asp Pro Val Ser Arg Thr Pro Ala Leu Val
            100                 105                 110

Phe Glu His Val Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu
        115                 120                 125

Thr Asp Tyr Asp Ile Arg Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu
    130                 135                 140

Asp Tyr Cys His Ser Met Gly Ile Met His Arg Asp Val Lys Pro His
145                 150                 155                 160

Asn Val Met Ile Asp His Glu His Arg Lys Leu Arg Leu Ile Asp Trp
                165                 170                 175

Gly Leu Ala Glu Phe Tyr His Pro Gly Gln Glu Tyr Asn Val Arg Val
            180                 185                 190

Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln Met
        195                 200                 205

Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala Ser
    210                 215                 220

Met Ile Phe Arg Lys Glu Pro Phe Phe His Gly His Asp Asn Tyr Asp
225                 230                 235                 240

Gln Leu Val Arg Ile Ala Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp
                245                 250                 255

Tyr Ile Asp Lys Tyr Asn Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile
            260                 265                 270

Leu Gly Arg His Ser Arg Lys Arg Trp Glu Arg Phe Val His Ser Glu
        275                 280                 285

Asn Gln His Leu Val Ser Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu
    290                 295                 300

Leu Arg Tyr Asp His Gln Ser Arg Leu Thr Ala Arg Glu Ala Met Glu
305                 310                 315                 320
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His Pro Tyr Phe Tyr Thr Val Val Lys Asp Gln Ala Arg Met Gly Ser
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Ser Ser Met Pro Gly Gly Ser Thr Pro Val Ser Ser Ala Asn Met Met
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Ser Gly Ile Ser Ser Val Pro Thr Pro Ser Pro Leu Gly Pro Leu Ala
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Gly Ser Pro Val Ile Ala Ala Ala Asn Pro Leu Gly Met Pro Val Pro
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Ala Ala Ala Gly Ala Gln Gln
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<220>
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<400> 12

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Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
             20                  25                  30

Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
         35                  40                  45
```

```
Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
     50                  55                  60

Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
 65                  70                  75                  80

Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
                85                  90                  95

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
            100                 105                 110

Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
        115                 120                 125

Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
    130                 135                 140

Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
145                 150                 155                 160

Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
                165                 170                 175

Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
            180                 185                 190

Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
        195                 200                 205

His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
    210                 215                 220

Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
225                 230                 235                 240

Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
                245                 250                 255

Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
            260                 265                 270

Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
        275                 280                 285

His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
    290                 295                 300

Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
305                 310                 315                 320

Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
                325                 330                 335

Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
            340                 345                 350

Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
        355                 360                 365
```

```
Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
    370                 375                 380

Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
385                 390                 395                 400

Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
                405                 410                 415

Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
            420                 425                 430

Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
        435                 440                 445

Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
    450                 455                 460

Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465                 470                 475                 480

Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
                485                 490                 495

Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
            500                 505                 510

Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
        515                 520                 525

Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
    530                 535                 540

Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
545                 550                 555                 560

Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
                565                 570                 575

Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
            580                 585                 590

Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
        595                 600                 605

Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys
    610                 615                 620

Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile
625                 630                 635                 640

Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp
                645                 650                 655

Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly
            660                 665                 670

Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg
        675                 680                 685
```

```
His Ile Ser Ile Gly Gly Lys Thr Cys Thr Leu Lys Ser Val Ser Asn
    690                 695                 700

Ser Ile Leu Glu Cys Tyr Thr Pro Ala Gln Thr Ile Ser Thr Glu Phe
705                 710                 715                 720

Ala Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ile Phe
                725                 730                 735

Ser Tyr Arg Glu Asp Pro Ile Val Tyr Glu Ile His Pro Thr Lys Ser
            740                 745                 750

Phe Ile Ser Thr Trp Trp Lys Glu Pro Leu Asn Ile Val Ser Phe Leu
        755                 760                 765

Phe Cys Phe Ala Ser Gly Gly Ser Thr Ile Thr Gly Val Gly Lys Asn
    770                 775                 780

Leu Asn Ser Val Ser Val Pro Arg Met Val Ile Asn Val His Glu Ala
785                 790                 795                 800

Gly Arg Asn Phe Thr Val Ala Cys Gln His Arg Ser Asn Ser Glu Ile
                805                 810                 815

Ile Cys Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln Leu Pro
            820                 825                 830

Leu Lys Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser Lys Tyr
        835                 840                 845

Phe Asp Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe Glu Lys
    850                 855                 860

Pro Val Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile Lys Gly
865                 870                 875                 880

Asn Asp Ile Asp Pro Glu Ala Val Lys Gly Glu Val Leu Lys Val Gly
                885                 890                 895

Asn Lys Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val Leu Cys
            900                 905                 910

Thr Val Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu
        915                 920                 925

Trp Lys Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln
    930                 935                 940

Pro Asp Gln Asn Phe Thr Gly Leu Ile Ala Gly Val Val Ser Ile Ser
945                 950                 955                 960

Thr Ala Leu Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg
                965                 970                 975

Lys Gln Ile Lys Asp Leu Gly Ser Glu Leu Val Arg Tyr Asp Ala Arg
            980                 985                 990

Val His Thr Pro His Leu Asp Arg Leu Val Ser Ala Arg Ser Val Ser
        995                1000                1005
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Pro Thr Thr Glu Met Val Ser Asn Glu Ser Val Asp Tyr Arg Ala Thr
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Phe Pro Glu Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg
1025                1030                1035                1040

Gln Val Gln Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu Thr Ser Gly
                1045                1050                1055

Asp Ser Asp Ile Ser Ser Pro Leu Leu Gln Asn Thr Val His Ile Asp
            1060                1065                1070

Leu Ser Ala Leu Asn Pro Glu Leu Val Gln Ala Val Gln His Val Val
        1075                1080                1085

Ile Gly Pro Ser Ser Leu Ile Val His Phe Asn Glu Val Ile Gly Arg
   1090                1095                1100

Gly His Phe Gly Cys Val Tyr His Gly Thr Leu Leu Asp Asn Asp Gly
1105                1110                1115                1120

Lys Lys Ile His Cys Ala Val Lys Ser Leu Asn Arg Ile Thr Asp Ile
                1125                1130                1135

Gly Glu Val Ser Gln Phe Leu Thr Glu Gly Ile Ile Met Lys Asp Phe
            1140                1145                1150

Ser His Pro Asn Val Leu Ser Leu Leu Gly Ile Cys Leu Arg Ser Glu
        1155                1160                1165

Gly Ser Pro Leu Val Val Leu Pro Tyr Met Lys His Gly Asp Leu Arg
   1170                1175                1180

Asn Phe Ile Arg Asn Glu Thr His Asn Pro Thr Val Lys Asp Leu Ile
1185                1190                1195                1200

Gly Phe Gly Leu Gln Val Ala Lys Ala Met Lys Tyr Leu Ala Ser Lys
                1205                1210                1215

Lys Phe Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Asp Glu
            1220                1225                1230

Lys Phe Thr Val Lys Val Ala Asp Phe Gly Leu Ala Arg Asp Met Tyr
        1235                1240                1245

Asp Lys Glu Tyr Tyr Ser Val His Asn Lys Thr Gly Ala Lys Leu Pro
   1250                1255                1260

Val Lys Trp Met Ala Leu Glu Ser Leu Gln Thr Gln Lys Phe Thr Thr
1265                1270                1275                1280

Lys Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp Glu Leu Met Thr
                1285                1290                1295

Arg Gly Ala Pro Pro Tyr Pro Asp Val Asn Thr Phe Asp Ile Thr Val
            1300                1305                1310

Tyr Leu Leu Gln Gly Arg Arg Leu Leu Gln Pro Glu Tyr Cys Pro Asp
        1315                1320                1325
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Pro Leu Tyr Glu Val Met Leu Lys Cys Trp His Pro Lys Ala Glu Met
   1330                1335                1340

Arg Pro Ser Phe Ser Glu Leu Val Ser Arg Ile Ser Ala Ile Phe Ser
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Thr Phe Ile Gly Glu His Tyr Val His Val Asn Ala Thr Tyr Val Asn
               1365                1370                1375

Val Lys Cys Val Ala Pro Tyr Pro Ser Leu Leu Ser Ser Glu Asp Asn
           1380                1385                1390

Ala Asp Asp Glu Val Asp Thr Arg Pro Ala Ser Phe Trp Glu Thr Ser
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<400> 13

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<213> Homo sapiens

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5'-3' exonuclease

<400> 14

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Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
         35                  40                  45

Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
     50                  55                  60

Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
 65                  70                  75                  80

Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
                 85                  90                  95

Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln
            100                 105                 110

Gln Ala Gln Ala Ala Gly Ala Glu Gln Glu Val Glu Lys Phe Thr Lys
        115                 120                 125

Arg Leu Val Lys Val Thr Lys Gln His Asn Asp Glu Cys Lys His Leu
    130                 135                 140
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Leu Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu
145                 150                 155                 160

Ala Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala
                165                 170                 175

Thr Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg
            180                 185                 190

His Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His
        195                 200                 205

Leu Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val
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Asp Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly
225                 230                 235                 240

Ile Gly Pro Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile
                245                 250                 255

Glu Glu Ile Val Arg Arg Leu Asp Pro Asn Lys Tyr Pro Val Pro Glu
            260                 265                 270

Asn Trp Leu His Lys Glu Ala His Gln Leu Phe Leu Glu Pro Glu Val
        275                 280                 285

Leu Asp Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu
    290                 295                 300

Glu Leu Ile Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg
305                 310                 315                 320

Ile Arg Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr
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Gln Gly Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser
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Ala Lys Arg Lys Glu Pro Glu Pro Lys Gly Ser Thr Lys Lys Lys Ala
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Lys Thr Gly Ala Ala Gly Lys Phe Lys Arg Gly Lys
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<212> DNA
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<212> PRT
<213> Homo sapiens

<220>
<223> REV1 dCMP transferase

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Phe Arg Ser Asp Ala Ala Met Gln Lys Asp Gly Thr Ser Ser Thr Ile
35 40 45

Phe Ser Gly Val Ala Ile Tyr Val Asn Gly Tyr Thr Asp Pro Ser Ala
50 55 60

Glu Glu Leu Arg Lys Leu Met Met Leu His Gly Gly Gln Tyr His Val
65 70 75 80

Tyr Tyr Ser Arg Ser Lys Thr Thr His Ile Ile Ala Thr Asn Leu Pro
85 90 95

Asn Ala Lys Ile Lys Glu Leu Lys Gly Glu Lys Val Ile Arg Pro Glu
100 105 110

Trp Ile Val Glu Ser Ile Lys Ala Gly Arg Leu Leu Ser Tyr Ile Pro
115 120 125

Tyr Gln Leu Tyr Thr Lys Gln Ser Ser Val Gln Lys Gly Leu Ser Phe
130 135 140

Asn Pro Val Cys Arg Pro Glu Asp Pro Leu Pro Gly Pro Ser Asn Ile
145 150 155 160

Ala Lys Gln Leu Asn Asn Arg Val Asn His Ile Val Lys Lys Ile Glu
165 170 175

Thr Glu Asn Glu Val Lys Val Asn Gly Met Asn Ser Trp Asn Glu Glu
180 185 190

Asp Glu Asn Asn Asp Phe Ser Phe Val Asp Leu Glu Gln Thr Ser Pro
195 200 205

Gly Arg Lys Gln Asn Gly Ile Pro His Pro Arg Gly Ser Thr Ala Ile
210 215 220

Phe Asn Gly His Thr Pro Ser Ser Asn Gly Ala Leu Lys Thr Gln Asp
225 230 235 240

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Cys Leu Val Pro Met Val Asn Ser Val Ala Ser Arg Leu Ser Pro Ala
                245                 250                 255

Phe Ser Gln Glu Glu Asp Lys Ala Glu Lys Ser Ser Thr Asp Phe Arg
            260                 265                 270

Asp Cys Thr Leu Gln Gln Leu Gln Gln Ser Thr Arg Asn Thr Asp Ala
        275                 280                 285

Leu Arg Asn Pro His Arg Thr Asn Ser Phe Ser Leu Ser Pro Leu His
    290                 295                 300

Ser Asn Thr Lys Ile Asn Gly Ala His His Ser Thr Val Gln Gly Pro
305                 310                 315                 320

Ser Ser Thr Lys Ser Thr Ser Ser Val Ser Thr Phe Ser Lys Ala Ala
                325                 330                 335

Pro Ser Val Pro Ser Lys Pro Ser Asp Cys Asn Phe Ile Ser Asn Phe
            340                 345                 350

Tyr Ser His Ser Arg Leu His His Ile Ser Met Trp Lys Cys Glu Leu
        355                 360                 365

Thr Glu Phe Val Asn Thr Leu Gln Arg Gln Ser Asn Gly Ile Phe Pro
    370                 375                 380

Gly Arg Glu Lys Leu Lys Lys Met Lys Thr Gly Arg Ser Ala Leu Val
385                 390                 395                 400

Val Thr Asp Thr Gly Asp Met Ser Val Leu Asn Ser Pro Arg His Gln
                405                 410                 415

Ser Cys Ile Met His Val Asp Met Asp Cys Phe Phe Val Ser Val Gly
            420                 425                 430

Ile Arg Asn Arg Pro Asp Leu Lys Gly Lys Pro Val Ala Val Thr Ser
        435                 440                 445

Asn Arg Gly Thr Gly Arg Ala Pro Leu Arg Pro Gly Ala Asn Pro Gln
    450                 455                 460

Leu Glu Trp Gln Tyr Tyr Gln Asn Lys Ile Leu Lys Gly Lys Ala Ala
465                 470                 475                 480

Asp Ile Pro Asp Ser Ser Leu Trp Glu Asn Pro Asp Ser Ala Gln Ala
                485                 490                 495

Asn Gly Ile Asp Ser Val Leu Ser Arg Ala Glu Ile Ala Ser Cys Ser
            500                 505                 510

Tyr Glu Ala Arg Gln Leu Gly Ile Lys Asn Gly Met Phe Phe Gly His
        515                 520                 525

Ala Lys Gln Leu Cys Pro Asn Leu Gln Ala Val Pro Tyr Asp Phe His
    530                 535                 540

Ala Tyr Lys Glu Val Ala Gln Thr Leu Tyr Glu Thr Leu Ala Ser Tyr
545                 550                 555                 560
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Thr His Asn Ile Glu Ala Val Ser Cys Asp Glu Ala Leu Val Asp Ile
                565                 570                 575

Thr Glu Ile Leu Ala Glu Thr Lys Leu Thr Pro Asp Glu Phe Ala Asn
            580                 585                 590

Ala Val Arg Met Glu Ile Lys Asp Gln Thr Lys Cys Ala Ala Ser Val
        595                 600                 605

Gly Ile Gly Ser Asn Ile Leu Leu Ala Arg Met Ala Thr Arg Lys Ala
    610                 615                 620

Lys Pro Asp Gly Gln Tyr His Leu Lys Pro Glu Glu Val Asp Asp Phe
625                 630                 635                 640

Ile Arg Gly Gln Leu Val Thr Asn Leu Pro Gly Val Gly His Ser Met
                645                 650                 655

Glu Ser Lys Leu Ala Ser Leu Gly Ile Lys Thr Cys Gly Asp Leu Gln
            660                 665                 670

Tyr Met Thr Met Ala Lys Leu Gln Lys Glu Phe Gly Pro Lys Thr Gly
        675                 680                 685

Gln Met Leu Tyr Arg Phe Cys Arg Gly Leu Asp Asp Arg Pro Val Arg
    690                 695                 700

Thr Glu Lys Glu Arg Lys Ser Val Ser Ala Glu Ile Asn Tyr Gly Ile
705                 710                 715                 720

Arg Phe Thr Gln Pro Lys Glu Ala Glu Ala Phe Leu Leu Ser Leu Ser
                725                 730                 735

Glu Glu Ile Gln Arg Arg Leu Glu Ala Thr Gly Met Lys Gly Lys Arg
            740                 745                 750

Leu Thr Leu Lys Ile Met Val Arg Lys Pro Gly Ala Pro Val Glu Thr
        755                 760                 765

Ala Lys Phe Gly Gly His Gly Ile Cys Asp Asn Ile Ala Arg Thr Val
    770                 775                 780

Thr Leu Asp Gln Ala Thr Asp Asn Ala Lys Ile Ile Gly Lys Ala Met
785                 790                 795                 800

Leu Asn Met Phe His Thr Met Lys Leu Asn Ile Ser Asp Met Arg Gly
                805                 810                 815

Val Gly Ile His Val Asn Gln Leu Val Pro Thr Asn Leu Asn Pro Ser
            820                 825                 830

Thr Cys Pro Ser Arg Pro Ser Val Gln Ser Ser His Phe Pro Ser Gly
        835                 840                 845

Ser Tyr Ser Val Arg Asp Val Phe Gln Val Gln Lys Ala Lys Lys Ser
    850                 855                 860

Thr Glu Glu Glu His Lys Glu Val Phe Arg Ala Ala Val Asp Leu Glu
865                 870                 875                 880
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Ile Ser Ser Ala Ser Arg Thr Cys Thr Phe Leu Pro Pro Phe Pro Ala
                885                 890                 895

His Leu Pro Thr Ser Pro Asp Thr Asn Lys Ala Glu Ser Ser Gly Lys
            900                 905                 910

Trp Asn Gly Leu His Thr Pro Val Ser Val Gln Ser Arg Leu Asn Leu
        915                 920                 925

Ser Ile Glu Val Pro Ser Pro Ser Gln Leu Asp Gln Ser Val Leu Glu
    930                 935                 940

Ala Leu Pro Pro Asp Leu Arg Glu Gln Val Glu Gln Val Cys Ala Val
945                 950                 955                 960

Gln Gln Ala Glu Ser His Gly Asp Lys Lys Lys Glu Pro Val Asn Gly
                965                 970                 975

Cys Asn Thr Gly Ile Leu Pro Gln Pro Val Gly Thr Val Leu Leu Gln
            980                 985                 990

Ile Pro Glu Pro Gln Glu Ser Asn Ser Asp Ala Gly Ile Asn Leu Ile
        995                1000                1005

Ala Leu Pro Ala Phe Ser Gln Val Asp Pro Glu Val Phe Ala Ala Leu
   1010                1015                1020

Pro Ala Glu Leu Gln Arg Glu Leu Lys Ala Ala Tyr Asp Gln Arg Gln
1025                1030                1035                1040

Arg Gln Gly Glu Asn Ser Thr His Gln Gln Ser Ala Ser Ala Ser Val
                1045                1050                1055

Pro Lys Asn Pro Leu Leu His Leu Lys Ala Ala Val Lys Glu Lys Lys
            1060                1065                1070

Arg Asn Lys Lys Lys Lys Thr Ile Gly Ser Pro Lys Arg Ile Gln Ser
        1075                1080                1085

Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala Lys Thr Leu Pro Gly
   1090                1095                1100

Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly Phe Leu Lys His Glu
1105                1110                1115                1120

Gly Pro Pro Ala Glu Lys Pro Leu Glu Glu Leu Ser Ala Ser Thr Ser
                1125                1130                1135

Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp Pro Ala Gly Cys Val
            1140                1145                1150

Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val Glu Phe Asn Asp Val
        1155                1160                1165

Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile Ser Asp Pro Met Glu
   1170                1175                1180

Glu Asp Ile Leu Gln Val Val Lys Tyr Cys Thr Asp Leu Ile Glu Glu
1185                1190                1195                1200
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Lys Asp Leu Glu Lys Leu Asp Leu Val Ile Lys Tyr Met Lys Arg Leu
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Met Gln Gln Ser Val Glu Ser Val Trp Asn Met Ala Phe Asp Phe Ile
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Lys Val Thr
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ggacaaggaa gggtacagtg gcgtgggcct gctttcccgc cagtgcccac tcaaagtttc 2040
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aattctgttt catttctata ggcgatgagg agcatgatca ggaaggccgg gtgattgtgg 2220
ctgaatttga ctcgtttgtg ctggtaacag catatgtacc taatgcaggc cgaggtctgg 2280

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ttcgcaaccc caaggggaac aaaaagaatg ctggcttcac gccacaagag cgccaaggct 2460
tcggggaatt actgcaggct gtgccactgg ctgacagctt taggcacctc taccccaaca 2520
caccctatgc ctacaccttt tggacttata tgatgaatgc tcgatccaag aatgttggtt 2580
ggcgccttga ttacttttg ttgtcccact ctctgttacc tgcattgtgt gacagcaaga 2640
tccgttccaa ggccctcggc agtgatcact gtcctatcac cctataccta gcactgtgac 2700
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aaacactctt cagagaaatc tgcattctat ttctcatgta taaaactagg aatcctccaa 2820
ccaggctcct gtgatagagt tcttttaagc ccaagatttt ttatttgagg gtttttttgtt 2880
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taaagagcca tagtttc                                                  2957
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<210> 18
<211> 318
<212> PRT
<213> Homo sapiens

<220>
<223> apyrimidinic endonuclease 1 (APE1), AP
endonuclease 1, HAP1

<400> 18

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Met Pro Lys Arg Gly Lys Lys Gly Ala Val Ala Glu Asp Gly Asp Glu
  1               5                  10                  15

Leu Arg Thr Glu Pro Glu Ala Lys Lys Ser Lys Thr Ala Ala Lys Lys
             20                  25                  30

Asn Asp Lys Glu Ala Ala Gly Glu Gly Pro Ala Leu Tyr Glu Asp Pro
         35                  40                  45

Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro Ala Thr Leu Lys Ile
     50                  55                  60

Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp Ile Lys Lys Lys Gly
 65                  70                  75                  80

Leu Asp Trp Val Lys Glu Glu Ala Pro Asp Ile Leu Cys Leu Gln Glu
                 85                  90                  95

Thr Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu Leu Gln Glu Leu Pro
            100                 105                 110

Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser Asp Lys Glu Gly Tyr
        115                 120                 125

Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro Leu Lys Val Ser Tyr
    130                 135                 140

Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly Arg Val Ile Val Ala
145                 150                 155                 160

Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr Val Pro Asn Ala Gly
                165                 170                 175

Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg Trp Asp Glu Ala Phe
            180                 185                 190
```

```
Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys Pro Leu Val Leu Cys
        195                 200                 205

Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp Leu Arg Asn Pro Lys
    210                 215                 220

Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln Glu Ala Gln Gly Phe
225                 230                 235                 240

Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp Ser Phe Arg His Leu
                245                 250                 255

Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp Thr Tyr Met Met Asn
            260                 265                 270

Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp Tyr Phe Leu Leu Ser
        275                 280                 285

His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys Ile Arg Ser Lys Ala
    290                 295                 300

Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr Leu Ala Leu
305                 310                 315
```

<210> 19
<211> 1161
<212> DNA
<213> Homo sapiens

<220>
<223> cyclin-dependent kinase 3 (CDK3), cyclin-dependent
protein kinase

<400> 19
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agagggcacc tatggggtgg tgtacaaggc caagaacagg gagacagggc agctggtggc 180
cctgaagaag atcagactgg atttggagat ggaggggtc ccaagcactg ccatcaggga 240
gatctcgctg ctcaaggaac tgaagcaccc caacatcgtc cgactgctgg acgtggtgca 300
caacgagagg aagctctatc tggtgtttga gttcctcagc caggacctga agaagtacat 360
ggactccacc ccaggctcag agctcccct gcacctcatc aagagctacc tcttccagct 420
gctgcagggg gtgagtttct gccactcaca tcgggtcatc caccgagacc tgaagcccca 480
gaacctgctc atcaatgagt tgggtgccat caagctggct gacttcggcc tggctcgcgc 540
cttcggggtg cccctgcgca cctacaccca tgaggtggtg acactgtggt atcgcgcccc 600
cgagattctc ttgggcagca agttctatac cacagctgtg gatatctgga gcattggttg 660
catctttgca gagatggtga ctcgaaaagc cctgtttcct ggtgactctg agattgacca 720
gctctttcgt atctttcgta tgctggggac acccagcgaa gacacatggc ccggggtcac 780
ccagctgcct gactataagg gcagcttccc taagtggacc aggaagggac tggaagagat 840
tgtgcccaat ctggagccag agggcaggga cctgctcatg caactcctgc agtatgaccc 900
cagccagcgg atcacagcca agactgccct ggcccacccg tacttctcat cccctgagcc 960
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agaggatgca tctggggaga gcaaagcact aaggaattca gcatcagcct gcagagggct 1140
gagtctgggt tagtcctgcc c                                          1161
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<210> 20
<211> 305
<212> PRT
<213> Homo sapiens

<220>
<223> cyclin-dependent kinase 3 (CDK3), cyclin-dependent protein kinase

<400> 20

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Met Asp Met Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
  1               5                  10                  15

Val Val Tyr Lys Ala Lys Asn Arg Glu Thr Gly Gln Leu Val Ala Leu
             20                  25                  30

Lys Lys Ile Arg Leu Asp Leu Glu Met Glu Gly Val Pro Ser Thr Ala
         35                  40                  45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Lys His Pro Asn Ile Val
     50                  55                  60

Arg Leu Leu Asp Val Val His Asn Glu Arg Lys Leu Tyr Leu Val Phe
 65                  70                  75                  80

Glu Phe Leu Ser Gln Asp Leu Lys Lys Tyr Met Asp Ser Thr Pro Gly
                 85                  90                  95

Ser Glu Leu Pro Leu His Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
            100                 105                 110

Gln Gly Val Ser Phe Cys His Ser His Arg Val Ile His Arg Asp Leu
        115                 120                 125

Lys Pro Gln Asn Leu Leu Ile Asn Glu Leu Gly Ala Ile Lys Leu Ala
    130                 135                 140

Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Leu Arg Thr Tyr Thr
145                 150                 155                 160

His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly
                165                 170                 175

Ser Lys Phe Tyr Thr Thr Ala Val Asp Ile Trp Ser Ile Gly Cys Ile
            180                 185                 190

Phe Ala Glu Met Val Thr Arg Lys Ala Leu Phe Pro Gly Asp Ser Glu
        195                 200                 205

Ile Asp Gln Leu Phe Arg Ile Phe Arg Met Leu Gly Thr Pro Ser Glu
    210                 215                 220

Asp Thr Trp Pro Gly Val Thr Gln Leu Pro Asp Tyr Lys Gly Ser Phe
225                 230                 235                 240

Pro Lys Trp Thr Arg Lys Gly Leu Glu Glu Ile Val Pro Asn Leu Glu
                245                 250                 255

Pro Glu Gly Arg Asp Leu Leu Met Gln Leu Leu Gln Tyr Asp Pro Ser
            260                 265                 270

Gln Arg Ile Thr Ala Lys Thr Ala Leu Ala His Pro Tyr Phe Ser Ser
        275                 280                 285
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Pro Glu Pro Ser Pro Ala Ala Arg Gln Tyr Val Leu Gln Arg Phe Arg
290 295 300

His
305

<210> 21
<211> 2297
<212> DNA
<213> Homo sapiens

<220>
<223> PIM1 oncogene serine threonine kinase

<400> 21
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cgcccgcgcc tgcaacgacc tgcacgccac caagctggcg ccgggcaagg agaaggagcc 120
cctggagtcg cagtaccagg tgggcccgct actgggcagc ggcggcttcg gctcggtcta 180
ctcaggcatc cgcgtctccg acaacttgcc ggtggccatc aaacacgtgg agaaggaccg 240
gatttccgac tggggagagc tgcctaatgg cactcgagtg cccatggaag tggtcctgct 300
gaagaaggtg agctcgggtt tctccggcgt cattaggctc ctggactggt tcgagaggcc 360
cgacagtttc gtcctgatcc tggagaggcc cgagccggtg caagatctct tcgacttcat 420
cacggaaagg ggagccctgc aagaggagct ggcccgcagc ttcttctggc aggtgctgga 480
ggccgtgcgg cactgccaca actgcggggt gctccaccgc gacatcaagg acgaaaacat 540
ccttatcgac ctcaatcgcg gcgagctcaa gctcatcgac ttcgggtcgg gggcgctgct 600
caaggacacc gtctacacgg acttcgatgg gacccgagtg tatagccctc cagagtggat 660
ccgctaccat cgctaccatg gcaggtcggc ggcagtctgg tccctgggga tcctgctgta 720
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<210> 22
<211> 313
<212> PRT
<213> Homo sapiens

<220>
<223> PIM1 oncogene serine threonine kinase

<400> 22
Met Leu Leu Ser Lys Ile Asn Ser Leu Ala His Leu Arg Ala Arg Ala
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Cys Asn Asp Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu
20 25 30

Pro Leu Glu Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly
35 40 45

Phe Gly Ser Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val
50 55 60

Ala Ile Lys His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu
65 70 75 80

Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val
85 90 95

Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg
100 105 110

Pro Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp
115 120 125

Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala
130 135 140

Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn
145 150 155 160

Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp
165 170 175

Leu Asn Arg Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu
180 185 190

Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser
195 200 205

Pro Pro Glu Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala
210 215 220

Val Trp Ser Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile
225 230 235 240

Pro Phe Glu His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg
245 250 255

Gln Arg Val Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala
260 265 270

Leu Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro
275 280 285

Trp Met Gln Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu
290 295 300

His Ser Leu Ser Pro Gly Pro Ser Lys
305 310

<210> 23
<211> 3178
<212> DNA
<213> Homo sapiens

<220>
<223> CDC7 cell division cycle 7 (CDC7), CDC7 cell division cycle 7-like 1 (CDC7L1) protein serine threonine kinase

<400> 23
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gtgttaaaaa agatattgag aagctttatg aagctgtacc acagcttagt aatgtgttta 300
agattgagga caaaattgga gaaggcactt tcagctctgt ttatttggcc acagcacagt 360
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ttaatctgtt caaagctttg aaacgcattc atcagtttgg tattgttcac cgtgatgtta 660
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aacatgatct tctttgagtt aaacctacct aagtagattt taggtgggtt cctattaggt 2100
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agatataatt aggtagctgc tgaaaggaaa agtgaataca gaattgacgg tattattgga 2760
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<210> 24
<211> 574
<212> PRT
<213> Homo sapiens

<220>
<223> CDC7 cell division cycle 7 (CDC7), CDC7 cell division cycle 7-like 1 (CDC7L1) protein serine threonine kinase

<400> 24

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Met Glu Ala Ser Leu Gly Ile Gln Met Asp Glu Pro Met Ala Phe Ser
  1               5                  10                  15

Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu
             20                  25                  30

Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr
         35                  40                  45

Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile
     50                  55                  60

Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln
 65                  70                  75                  80

Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile Pro Thr Ser
                 85                  90                  95

His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr Val Ala Gly
            100                 105                 110

Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg Lys Asn Asp
        115                 120                 125

His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser Phe Leu Asp
    130                 135                 140

Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr Met Leu Asn
145                 150                 155                 160

Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile Val His Arg
                165                 170                 175

Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu Lys Lys Tyr
            180                 185                 190

Ala Leu Val Asp Phe Gly Leu Ala Gln Gly Thr His Asp Thr Lys Ile
        195                 200                 205
```

```
Glu Leu Leu Lys Phe Val Gln Ser Glu Ala Gln Gln Glu Arg Cys Ser
    210                 215                 220

Gln Asn Lys Ser His Ile Ile Thr Gly Asn Lys Ile Pro Leu Ser Gly
225                 230                 235                 240

Pro Val Pro Lys Glu Leu Asp Gln Gln Ser Thr Thr Lys Ala Ser Val
                245                 250                 255

Lys Arg Pro Tyr Thr Asn Ala Gln Ile Gln Ile Lys Gln Gly Lys Asp
            260                 265                 270

Gly Lys Glu Gly Ser Val Gly Leu Ser Val Gln Arg Ser Val Phe Gly
        275                 280                 285

Glu Arg Asn Phe Asn Ile His Ser Ser Ile Ser His Glu Ser Pro Ala
    290                 295                 300

Val Lys Leu Met Lys Gln Ser Lys Thr Val Asp Val Leu Ser Arg Lys
305                 310                 315                 320

Leu Ala Thr Lys Lys Lys Ala Ile Ser Thr Lys Val Met Asn Ser Ala
                325                 330                 335

Val Met Arg Lys Thr Ala Ser Ser Cys Pro Ala Ser Leu Thr Cys Asp
            340                 345                 350

Cys Tyr Ala Thr Asp Lys Val Cys Ser Ile Cys Leu Ser Arg Arg Gln
        355                 360                 365

Gln Val Ala Pro Arg Ala Gly Thr Pro Gly Phe Arg Ala Pro Glu Val
    370                 375                 380

Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met Trp Ser Ala
385                 390                 395                 400

Gly Val Ile Phe Leu Ser Leu Leu Ser Gly Arg Tyr Pro Phe Tyr Lys
                405                 410                 415

Ala Ser Asp Asp Leu Thr Ala Leu Ala Gln Ile Met Thr Ile Arg Gly
            420                 425                 430

Ser Arg Glu Thr Ile Gln Ala Ala Lys Thr Phe Gly Lys Ser Ile Leu
        435                 440                 445

Cys Ser Lys Glu Val Pro Ala Gln Asp Leu Arg Lys Leu Cys Glu Arg
    450                 455                 460

Leu Arg Gly Met Asp Ser Ser Thr Pro Lys Leu Thr Ser Asp Ile Gln
465                 470                 475                 480

Gly His Ala Ser His Gln Pro Ala Ile Ser Glu Lys Thr Asp His Lys
                485                 490                 495

Ala Ser Cys Leu Val Gln Thr Pro Pro Gly Gln Tyr Ser Gly Asn Ser
            500                 505                 510

Phe Lys Lys Gly Asp Ser Asn Ser Cys Glu His Cys Phe Asp Glu Tyr
        515                 520                 525
```

```
Asn Thr Asn Leu Glu Gly Trp Asn Glu Val Pro Asp Glu Ala Tyr Asp
    530                 535                 540

Leu Leu Asp Lys Leu Leu Asp Leu Asn Pro Ala Ser Arg Ile Thr Ala
545                 550                 555                 560

Glu Glu Ala Leu Leu His Pro Phe Phe Lys Asp Met Ser Leu
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<210> 25
<211> 1427
<212> DNA
<213> Homo sapiens

<220>
<223> cyclin-dependent kinase 7 (CDK7), kinase subunit
of Cdk-activating kinase (CAK), kinase component
of transcription factor complex TFIIH

<400> 25
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<210> 26
<211> 346
<212> PRT
<213> Homo sapiens

<220>
<223> cyclin-dependent kinase 7 (CDK7), kinase subunit
of Cdk-activating kinase (CAK), kinase component
of transcription factor complex TFIIH

<400> 26
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Met Ala Leu Asp Val Lys Ser Arg Ala Lys Arg Tyr Glu Lys Leu Asp
  1               5                  10                  15
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Phe Leu Gly Glu Gly Gln Phe Ala Thr Val Tyr Lys Ala Arg Asp Lys
            20                  25                  30

Asn Thr Asn Gln Ile Val Ala Ile Lys Lys Ile Lys Leu Gly His Arg
        35                  40                  45

Ser Glu Ala Lys Asp Gly Ile Asn Arg Thr Ala Leu Arg Glu Ile Lys
    50                  55                  60

Leu Leu Gln Glu Leu Ser His Pro Asn Ile Ile Gly Leu Leu Asp Ala
65                  70                  75                  80

Phe Gly His Lys Ser Asn Ile Ser Leu Val Phe Asp Phe Met Glu Thr
                85                  90                  95

Asp Leu Glu Val Ile Ile Lys Asp Asn Ser Leu Val Leu Thr Pro Ser
            100                 105                 110

His Ile Lys Ala Tyr Met Leu Met Thr Leu Gln Gly Leu Glu Tyr Leu
        115                 120                 125

His Gln His Trp Ile Leu His Arg Asp Leu Lys Pro Asn Asn Leu Leu
    130                 135                 140

Leu Asp Glu Asn Gly Val Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys
145                 150                 155                 160

Ser Phe Gly Ser Pro Asn Arg Ala Tyr Thr His Gln Val Val Thr Arg
                165                 170                 175

Trp Tyr Arg Ala Pro Glu Leu Leu Phe Gly Ala Arg Met Tyr Gly Val
            180                 185                 190

Gly Val Asp Met Trp Ala Val Gly Cys Ile Leu Ala Glu Leu Leu Leu
        195                 200                 205

Arg Val Pro Phe Leu Pro Gly Asp Ser Asp Leu Asp Gln Leu Thr Arg
    210                 215                 220

Ile Phe Glu Thr Leu Gly Thr Pro Thr Glu Glu Gln Trp Pro Asp Met
225                 230                 235                 240

Cys Ser Leu Pro Asp Tyr Val Thr Phe Lys Ser Phe Pro Gly Ile Pro
                245                 250                 255

Leu His His Ile Phe Ser Ala Ala Gly Asp Asp Leu Leu Asp Leu Ile
            260                 265                 270

Gln Gly Leu Phe Leu Phe Asn Pro Cys Ala Arg Ile Thr Ala Thr Gln
        275                 280                 285

Ala Leu Lys Met Lys Tyr Phe Ser Asn Arg Pro Gly Pro Thr Pro Gly
    290                 295                 300

Cys Gln Leu Pro Arg Pro Asn Cys Pro Val Glu Thr Leu Lys Glu Gln
305                 310                 315                 320
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Ser Asn Pro Ala Leu Ala Ile Lys Arg Lys Arg Thr Glu Ala Leu Glu
325 330 335

Gln Gly Gly Leu Pro Lys Lys Leu Ile Phe
340 345

<210> 27
<211> 2169
<212> DNA
<213> Homo sapiens

<220>
<223> cytokine-inducible kinase (CNK) serine threonine kinase, proliferation-related kinase (PRK), polo-like kinase 3 (PLK3)

<400> 27
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aattttgca 2169

<210> 28
<211> 607
<212> PRT
<213> Homo sapiens

<220>
<223> cytokine-inducible kinase (CNK) serine threonine kinase, proliferation-related kinase (PRK), polo-like kinase 3 (PLK3)

<400> 28

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Pro Arg Ser Gly Arg Thr Tyr Leu Lys Gly Arg Leu Leu Gly Lys Gly
             20                  25                  30

Gly Phe Ala Arg Cys Tyr Glu Ala Thr Asp Thr Glu Thr Gly Ser Ala
         35                  40                  45

Tyr Ala Val Lys Val Ile Pro Gln Ser Arg Val Ala Lys Pro His Gln
     50                  55                  60

Arg Glu Lys Ile Leu Asn Glu Ile Glu Leu His Arg Asp Leu Gln His
 65                  70                  75                  80

Arg His Ile Val Arg Phe Ser His His Phe Glu Asp Ala Asp Asn Ile
                 85                  90                  95

Tyr Ile Phe Leu Glu Leu Cys Ser Arg Lys Ser Leu Ala His Ile Trp
            100                 105                 110

Lys Ala Arg His Thr Leu Leu Glu Pro Glu Val Arg Tyr Tyr Leu Arg
        115                 120                 125

Gln Ile Leu Ser Gly Leu Lys Tyr Leu His Gln Arg Gly Ile Leu His
    130                 135                 140

Arg Asp Leu Lys Leu Gly Asn Phe Phe Ile Thr Glu Asn Met Glu Leu
145                 150                 155                 160

Lys Val Gly Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Pro Glu Gln
                165                 170                 175

Arg Lys Lys Thr Ile Cys Gly Thr Pro Asn Tyr Val Ala Pro Glu Val
            180                 185                 190

Leu Leu Arg Gln Gly His Gly Pro Glu Ala Asp Val Trp Ser Leu Gly
        195                 200                 205

Cys Val Met Tyr Thr Leu Leu Cys Gly Ser Pro Pro Phe Glu Thr Ala
    210                 215                 220

Asp Leu Lys Glu Thr Tyr Arg Cys Ile Lys Gln Val His Tyr Thr Leu
225                 230                 235                 240

Pro Ala Ser Leu Ser Leu Pro Ala Arg Gln Leu Leu Ala Ala Ile Leu
                245                 250                 255

Arg Ala Ser Pro Arg Asp Arg Pro Ser Ile Asp Gln Ile Leu Arg His
            260                 265                 270

Asp Phe Phe Thr Lys Gly Tyr Thr Pro Asp Arg Leu Pro Ile Ser Ser
        275                 280                 285
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Cys Val Thr Val Pro Asp Leu Thr Pro Pro Asn Pro Ala Arg Ser Leu
    290                 295                 300

Phe Ala Lys Val Thr Lys Ser Leu Phe Gly Arg Lys Lys Lys Ser Lys
305                 310                 315                 320

Asn His Ala Gln Glu Arg Asp Glu Val Ser Gly Leu Val Ser Gly Leu
                325                 330                 335

Met Arg Thr Ser Val Gly His Gln Asp Ala Arg Pro Glu Ala Pro Ala
            340                 345                 350

Ala Ser Gly Pro Ala Pro Val Ser Leu Val Glu Thr Ala Pro Glu Asp
        355                 360                 365

Ser Ser Pro Arg Gly Thr Leu Ala Ser Ser Gly Asp Gly Phe Glu Glu
    370                 375                 380

Gly Leu Thr Val Ala Thr Val Val Glu Ser Ala Leu Cys Ala Leu Arg
385                 390                 395                 400

Asn Cys Ile Ala Phe Met Pro Pro Ala Glu Gln Asn Pro Ala Pro Leu
                405                 410                 415

Ala Gln Pro Glu Pro Leu Val Trp Val Ser Lys Trp Val Asp Tyr Ser
            420                 425                 430

Asn Lys Phe Gly Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val
        435                 440                 445

Leu Phe Asn Asp Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr
    450                 455                 460

Val His Tyr Asn Pro Thr Ser Thr Lys His Phe Ser Phe Ser Val Gly
465                 470                 475                 480

Ala Val Pro Arg Ala Leu Gln Pro Gln Leu Gly Ile Leu Arg Tyr Phe
                485                 490                 495

Ala Ser Tyr Met Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser
            500                 505                 510

Val Glu Glu Val Glu Val Pro Ala Pro Pro Leu Leu Leu Gln Trp Val
        515                 520                 525

Lys Thr Asp Gln Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln
    530                 535                 540

Val Asn Phe Tyr Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu
545                 550                 555                 560

Pro Leu Leu Val Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr
                565                 570                 575

Leu Ala Ser His Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln
            580                 585                 590

Arg Leu Arg Tyr Ala Leu Arg Leu Leu Arg Asp Arg Ser Pro Ala
        595                 600                 605
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<210> 29
<211> 1321
<212> DNA
<213> Homo sapiens

<220>
<223> potentially prenylated protein tyrosine
phosphatase (PRL-3), protein tyrosine phosphatase
type IVA, member 3, isoform 2, transcript variant
2 (PTP4A3)

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a 1321

<210> 30
<211> 148
<212> PRT
<213> Homo sapiens

<220>
<223> potentially prenylated protein tyrosine
phosphatase (PRL-3), protein tyrosine phosphatase
type IVA, member 3, isoform 2, transcript variant
2 (PTP4A3)

<400> 30
Met Ala Arg Met Asn Arg Pro Ala Pro Val Glu Val Ser Tyr Lys His
1 5 10 15

Met Arg Phe Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Ser Thr
20 25 30

Phe Ile Glu Asp Leu Lys Lys Tyr Gly Ala Thr Thr Val Val Arg Val
35 40 45

Cys Glu Val Thr Tyr Asp Lys Thr Pro Leu Glu Lys Asp Gly Ile Thr
50 55 60

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Val Val Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Gly Lys Val
 65                  70                  75                  80

Val Glu Asp Trp Leu Ser Leu Val Lys Ala Lys Phe Cys Glu Ala Pro
                85                  90                  95

Gly Ser Cys Val Ala Val His Cys Val Ala Gly Leu Gly Arg Lys Arg
            100                 105                 110

Arg Gly Ala Ile Asn Ser Lys Gln Leu Thr Tyr Leu Glu Lys Tyr Arg
        115                 120                 125

Pro Lys Gln Arg Leu Arg Phe Lys Asp Pro His Thr His Lys Thr Arg
    130                 135                 140

Cys Cys Val Met
145
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<210> 31
<211> 3696
<212> DNA
<213> Homo sapiens

<220>
<223> serine threonine kinase 2 (STK2, NEK4)

<400> 31

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cccgctgccc tacccgccgc tgccgccgca tcccgactct gggccagcgc tgggaacatg 180
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<210> 32
<211> 841
<212> PRT
<213> Homo sapiens

<220>
<223> serine threonine kinase 2 (STK2, NEK4)

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Tyr Gly Glu Val Thr Leu Val Lys His Arg Arg Asp Gly Lys Gln Tyr
20 25 30

Val Ile Lys Lys Leu Asn Leu Arg Asn Ala Ser Ser Arg Glu Arg Arg
35 40 45

Ala Ala Glu Gln Glu Ala Gln Leu Leu Ser Gln Leu Lys His Pro Asn
50 55 60

Ile Val Thr Tyr Lys Glu Ser Trp Glu Gly Gly Asp Gly Leu Leu Tyr
65 70 75 80

Ile Val Met Gly Phe Cys Glu Gly Gly Asp Leu Tyr Arg Lys Leu Lys
85 90 95

Glu Gln Lys Gly Gln Leu Leu Pro Glu Asn Gln Val Val Glu Trp Phe
100 105 110

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Val Gln Ile Ala Met Ala Leu Gln Tyr Leu His Glu Lys His Ile Leu
        115                 120                 125

His Arg Asp Leu Lys Thr Gln Asn Val Phe Leu Thr Arg Thr Asn Ile
    130                 135                 140

Ile Lys Val Gly Asp Leu Gly Ile Ala Arg Val Leu Glu Asn His Cys
145                 150                 155                 160

Asp Met Ala Ser Thr Leu Ile Gly Thr Pro Tyr Tyr Met Ser Pro Glu
                165                 170                 175

Leu Phe Ser Asn Lys Pro Tyr Asn Tyr Lys Ser Asp Val Trp Ala Leu
            180                 185                 190

Gly Cys Cys Val Tyr Glu Met Ala Thr Leu Lys His Ala Phe Asn Ala
        195                 200                 205

Lys Asp Met Asn Ser Leu Val Tyr Arg Ile Ile Glu Gly Lys Leu Pro
    210                 215                 220

Pro Met Pro Arg Asp Tyr Ser Pro Glu Leu Ala Glu Leu Ile Arg Thr
225                 230                 235                 240

Met Leu Ser Lys Arg Pro Glu Glu Arg Pro Ser Val Arg Ser Ile Leu
                245                 250                 255

Arg Gln Pro Tyr Ile Lys Arg Gln Ile Ser Phe Phe Leu Glu Ala Thr
            260                 265                 270

Lys Ile Lys Thr Ser Lys Asn Asn Ile Lys Asn Gly Asp Ser Gln Ser
        275                 280                 285

Lys Pro Phe Ala Thr Val Val Ser Gly Glu Ala Glu Ser Asn His Glu
    290                 295                 300

Val Ile His Pro Gln Pro Leu Ser Ser Glu Gly Ser Gln Thr Tyr Ile
305                 310                 315                 320

Met Gly Glu Gly Lys Cys Leu Ser Gln Glu Lys Pro Arg Ala Ser Gly
                325                 330                 335

Leu Leu Lys Ser Pro Ala Ser Leu Lys Ala His Thr Cys Lys Gln Asp
            340                 345                 350

Leu Ser Asn Thr Thr Glu Leu Ala Thr Ile Ser Ser Val Asn Ile Asp
        355                 360                 365

Ile Leu Pro Ala Lys Gly Arg Asp Ser Val Ser Asp Gly Phe Val Gln
    370                 375                 380

Glu Asn Gln Pro Arg Tyr Leu Asp Ala Ser Asn Glu Leu Gly Gly Ile
385                 390                 395                 400

Cys Ser Ile Ser Gln Val Glu Glu Glu Met Leu Gln Asp Asn Thr Lys
                405                 410                 415

Ser Ser Ala Gln Pro Glu Asn Leu Ile Pro Met Trp Ser Ser Asp Ile
            420                 425                 430
```

```
Val Thr Gly Glu Lys Asn Glu Pro Val Lys Pro Leu Gln Pro Leu Ile
        435                 440                 445

Lys Glu Gln Lys Pro Lys Asp Gln Ser Leu Ala Leu Ser Pro Lys Leu
    450                 455                 460

Glu Cys Ser Gly Thr Ile Leu Ala His Ser Asn Leu Arg Leu Leu Gly
465                 470                 475                 480

Ser Ser Asp Ser Pro Ala Ser Ala Ser Arg Val Ala Gly Ile Thr Gly
                485                 490                 495

Val Cys His His Ala Gln Asp Gln Val Ala Gly Glu Cys Ile Ile Glu
            500                 505                 510

Lys Gln Gly Arg Ile His Pro Asp Leu Gln Pro His Asn Ser Gly Ser
        515                 520                 525

Glu Pro Ser Leu Ser Arg Gln Arg Arg Gln Lys Arg Arg Glu Gln Thr
    530                 535                 540

Glu His Arg Gly Glu Lys Arg Gln Val Arg Arg Asp Leu Phe Ala Phe
545                 550                 555                 560

Gln Glu Ser Pro Pro Arg Phe Leu Pro Ser His Pro Ile Val Gly Lys
                565                 570                 575

Val Asp Val Thr Ser Thr Gln Lys Glu Ala Glu Asn Gln Arg Arg Val
            580                 585                 590

Val Thr Gly Ser Val Ser Ser Ser Arg Ser Ser Glu Met Ser Ser Ser
        595                 600                 605

Lys Asp Arg Pro Leu Ser Ala Arg Glu Arg Arg Arg Leu Lys Gln Ser
    610                 615                 620

Gln Glu Glu Met Ser Ser Ser Gly Pro Ser Val Arg Lys Ala Ser Leu
625                 630                 635                 640

Ser Val Ala Gly Pro Gly Lys Pro Gln Glu Glu Asp Gln Pro Leu Pro
                645                 650                 655

Ala Arg Arg Leu Ser Ser Asp Cys Ser Val Thr Gln Glu Arg Lys Gln
            660                 665                 670

Ile His Cys Leu Ser Glu Asp Glu Leu Ser Ser Ser Thr Ser Ser Thr
        675                 680                 685

Asp Lys Ser Asp Gly Asp Tyr Gly Glu Gly Lys Gly Gln Thr Asn Glu
    690                 695                 700

Ile Asn Ala Leu Val Gln Leu Met Thr Gln Thr Leu Lys Leu Asp Ser
705                 710                 715                 720

Lys Glu Ser Cys Glu Asp Val Pro Val Ala Asn Pro Val Ser Glu Phe
                725                 730                 735

Lys Leu His Arg Lys Tyr Arg Asp Thr Leu Ile Leu His Gly Lys Val
            740                 745                 750
```

```
Ala Glu Glu Ala Glu Glu Ile His Phe Lys Glu Leu Pro Ser Ala Ile
        755                 760                 765

Met Pro Gly Ser Glu Lys Ile Arg Arg Leu Val Glu Val Leu Arg Thr
    770                 775                 780

Asp Val Ile Arg Gly Leu Gly Val Gln Leu Leu Glu Gln Val Tyr Asp
785                 790                 795                 800

Leu Leu Glu Glu Glu Asp Glu Phe Asp Arg Glu Val Arg Leu Arg Glu
                805                 810                 815

His Met Gly Glu Lys Tyr Thr Thr Tyr Ser Val Lys Ala Arg Gln Leu
            820                 825                 830

Lys Phe Phe Glu Glu Asn Met Asn Phe
        835                 840
```

<210> 33
<211> 1513
<212> DNA
<213> Homo sapiens

<220>
<223> serine threonine protein kinase NKIAMRE,
mitogen-activated protein kinase/cyclin-dependent
kinase-related protein kinase NKIATRE homologue

<400> 33

```
atggagatgt atgaaaccct tggaaaagtg ggagagggaa gttacggaac agtcatgaaa 60
tgtaaacata agaatactgg gcagatagtg gccattaaga tattttatga gagaccagaa 120
caatctgtca acaaaattgc gatgagagaa ataaagtttc taaagcaatt tcatcacgaa 180
aacctggtca atctgattga agtttttaga cagaaaaaga aaattcattt ggtatttgaa 240
tttattgacc acacagtatt agatgagtta caacattatt gtcatggact agagagtaag 300
cgacttagaa aatacctctt ccagatcctt cgagcaattg actatcttca cagtaataat 360
atcattcatc gagatataaa acctgagaat attttagtat cccagtcagg aattactaag 420
ctctgtgatt ttggttttgc acgaacacta gcagctcctg gggacattta tacggactat 480
gtggccacac gctggtatag agctcccgaa ttagtattaa aagatacttc ttatggaaaa 540
cctgtggata tctgggcttt gggctgtatg atcattgaga tggccactgg aaatccctat 600
cttcctagta gttctgattt ggatttactc cataaaattg ttttgaaagt gggcaatttg 660
tcacctcact tgcagaatat cttttccaag agccccattt ttgctggggt agttcttcct 720
caagttcaac accccaaaaa tgcaagaaaa aaatatccaa agcttaatgg attgttggca 780
gatatagttc atgcttgttt acaaattgat cctgctgaca ggatatcatc tagtgatctt 840
ttgcatcatg agtattttac tagagatgga tttattgaaa aattcatgcc agaactgaaa 900
gctaaattac tgcaggaagc aaaagtcaat tcattaataa agccaaaaga gagttctaaa 960
gaaaatgaac tcaggaaaga tgaaagaaaa acagtttata ccaatacact gctaagtagt 1020
tcagttttgg gagaggaaat agaaaaagag aaaaagccca aggagatcaa agtcagagtt 1080
attaaagtca aaggaggaag aggagatatc tcagaaccaa aaaagaaaga gtatgaaggt 1140
ggacttggtc aacaggatgc aaatgaaaat gttcatccta tgtctccaga tacaaaactt 1200
gtaaccattg aaccaccaaa ccctatcaat cccagcacta actgtaatgg cttgaaagaa 1260
aatccacatt gcggaggttc tgtaacaatg ccacccatca atctaactaa cagtaatttg 1320
atggctgcaa atctcagttc aaatctcttt caccccagtg tgaggtgagc tgtaacagag 1380
aagaaaccta aataatacaa cattcctgta taatggtatt tcaaagaatc gtgttcatag 1440
tgtctgtatg taaactgaac ttgaagaaaa tatattgaaa ttaaagctgt ataatgggcc 1500
aaaaaaaaaa aaa                                                    1513
```

<210> 34
<211> 455
<212> PRT
<213> Homo sapiens

<220>
<223> serine threonine protein kinase NKIAMRE,
mitogen-activated protein kinase/cyclin-dependent
kinase-related protein kinase NKIATRE homologue

<400> 34

```
Met Glu Met Tyr Glu Thr Leu Gly Lys Val Gly Glu Gly Ser Tyr Gly
  1               5                  10                  15

Thr Val Met Lys Cys Lys His Lys Asn Thr Gly Gln Ile Val Ala Ile
             20                  25                  30

Lys Ile Phe Tyr Glu Arg Pro Glu Gln Ser Val Asn Lys Ile Ala Met
         35                  40                  45

Arg Glu Ile Lys Phe Leu Lys Gln Phe His His Glu Asn Leu Val Asn
     50                  55                  60

Leu Ile Glu Val Phe Arg Gln Lys Lys Lys Ile His Leu Val Phe Glu
 65                  70                  75                  80

Phe Ile Asp His Thr Val Leu Asp Glu Leu Gln His Tyr Cys His Gly
                 85                  90                  95

Leu Glu Ser Lys Arg Leu Arg Lys Tyr Leu Phe Gln Ile Leu Arg Ala
            100                 105                 110

Ile Asp Tyr Leu His Ser Asn Asn Ile Ile His Arg Asp Ile Lys Pro
        115                 120                 125

Glu Asn Ile Leu Val Ser Gln Ser Gly Ile Thr Lys Leu Cys Asp Phe
    130                 135                 140

Gly Phe Ala Arg Thr Leu Ala Ala Pro Gly Asp Ile Tyr Thr Asp Tyr
145                 150                 155                 160

Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Val Leu Lys Asp Thr
                165                 170                 175

Ser Tyr Gly Lys Pro Val Asp Ile Trp Ala Leu Gly Cys Met Ile Ile
            180                 185                 190

Glu Met Ala Thr Gly Asn Pro Tyr Leu Pro Ser Ser Ser Asp Leu Asp
        195                 200                 205

Leu Leu His Lys Ile Val Leu Lys Val Gly Asn Leu Ser Pro His Leu
    210                 215                 220

Gln Asn Ile Phe Ser Lys Ser Pro Ile Phe Ala Gly Val Val Leu Pro
225                 230                 235                 240

Gln Val Gln His Pro Lys Asn Ala Arg Lys Lys Tyr Pro Lys Leu Asn
                245                 250                 255

Gly Leu Leu Ala Asp Ile Val His Ala Cys Leu Gln Ile Asp Pro Ala
            260                 265                 270
```

```
Asp Arg Ile Ser Ser Ser Asp Leu Leu His His Glu Tyr Phe Thr Arg
        275                 280                 285

Asp Gly Phe Ile Glu Lys Phe Met Pro Glu Leu Lys Ala Lys Leu Leu
    290                 295                 300

Gln Glu Ala Lys Val Asn Ser Leu Ile Lys Pro Lys Glu Ser Ser Lys
305                 310                 315                 320

Glu Asn Glu Leu Arg Lys Asp Glu Arg Lys Thr Val Tyr Thr Asn Thr
                325                 330                 335

Leu Leu Ser Ser Ser Val Leu Gly Glu Glu Ile Glu Lys Glu Lys Lys
            340                 345                 350

Pro Lys Glu Ile Lys Val Arg Val Ile Lys Val Lys Gly Gly Arg Gly
        355                 360                 365

Asp Ile Ser Glu Pro Lys Lys Lys Glu Tyr Glu Gly Gly Leu Gly Gln
    370                 375                 380

Gln Asp Ala Asn Glu Asn Val His Pro Met Ser Pro Asp Thr Lys Leu
385                 390                 395                 400

Val Thr Ile Glu Pro Pro Asn Pro Ile Asn Pro Ser Thr Asn Cys Asn
                405                 410                 415

Gly Leu Lys Glu Asn Pro His Cys Gly Gly Ser Val Thr Met Pro Pro
            420                 425                 430

Ile Asn Leu Thr Asn Ser Asn Leu Met Ala Ala Asn Leu Ser Ser Asn
        435                 440                 445

Leu Phe His Pro Ser Val Arg
    450                 455
```

<210> 35
<211> 3504
<212> DNA
<213> Homo sapiens

<220>
<223> HBO1 histone acetyltransferase, MYST histone acetyltransferase 2 (MYST2)

<400> 35
```
gccgctgccc gaatcggaac cgtcgggccg cagccgccgg caatgccgcg aaggaagagg 60
aatgcaggca gtagttcaga tggaaccgaa gattccgatt tttctacaga tctcgagcac 120
acagacagtt cagaaagtga tggcacatcc cgacgatctg ctcgagtcac ccgctcctca 180
gccaggctaa gccagagttc tcaagattcc agtcctgttc gaaatctgca gtcttttggc 240
actgaggagc ctgcttactc taccagaaga gtgacccgta gtcagcagca gcctacccca 300
gtgacaccga aaaaataccc tcttcggcag actcgttcat ctggttcaga aactgagcaa 360
gtggttgatt tttcagatag agaaactaaa aatacagctg atcatgatga gtcaccgcct 420
cgaactccaa ctggaaatgc gccttcttct gagtctgaca tagatatctc cagccccaat 480
gtatctcacg atgagagcat tgccaaggac atgtccctga aggactcagg cagtgatctc 540
tctcatcgcc ccaagcgccg tcgcttccat gaaagctaca acttcaatat gaagtgtcct 600
acaccaggct gtaactctct aggacacctt acaggaaaac atgagagaca tttctccatc 660
tcaggatgcc cactgtatca taacctctca gctgacgaat gcaaggtgag agcacagagc 720
cgggataagc agatagaaga aaggatgctg tctcacaggc aagatgacaa caacaggcat 780
gcaaccaggc accaggcacc aacggagagg cagcttcgat ataaggaaaa agtggctgaa 840
```

```
ctcaggaaga aaagaaattc tggactgagc aaagaacaga aagagaaata tatggaacac 900
agacagacct atgggaacac acgggaacct cttttagaaa acctgacaag cgagtatgac 960
ttggatcttt tccgaagagc acaagcccgg gcttcagagg atttggagaa gttaaggctg 1020
caaggccaaa tcacagaggg aagcaacatg attaaaacaa ttgcttttgg ccgctatgag 1080
cttgatacct ggtatcattc tccatatcct gaagaatatg cacggctggg acgtctctat 1140
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aaatgtgtgt ggaaacaccc acctggtgat gagatatatc gcaaaggttc aatctctgtg 1260
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ggcaagatgc ttattgattt cagttatttg ctttccaaag tcgaagaaaa agttggctcc 1560
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cttctccgct acctgcataa ttttcaaggc aaagagattt ctatcaaaga aatcagtcag 1680
gagacggctg tgaatcctgt ggacattgtc agcactctgc aagcccttca gatgctcaaa 1740
tactggaagg gaaaacacct agttttaaag agacaggacc tgattgatga gtggatagcc 1800
aaagaggcca aaaggtccaa ctccaataaa accatggatc ccagctgctt aaaatggacc 1860
cctcccaagg gcacttaaag tgacctgtca ttccgagcca gcgaacccca gcagtaggaa 1920
tccgtaccct agggatctgt ctgtcatttc tctgttgctc ttgtgattgg caagtacagt 1980
atcctttggg aaggccatcc ccctcaggac tgtcctggct ccgacctttg tgtacactgc 2040
agacgctggt tctgaggaac tgttgtttcg gcctcagtga ggttgcctgg atgggatctg 2100
tattagactt gagtgcaggt ctctcagcac tgacccaagg agttctgtta tggtactgta 2160
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taaatttctt cattttgatt aagagacctc tttttgatct gtattgggct aaccagagcc 2460
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cagcccatga ctcagcaagg cagaatggcc acccctgcca aagtttgctt ctcttttcaa 2940
cagtgcctca ccctccctct aggattaaag tgcttctgcc cttccacgaa ctcctcctcc 3000
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tgtcttcatg tggagccctc accacaatcc ctgactccgg tcatttgtgc ctttctcttg 3240
tcatctctgt acactactta tattcactgt gggttggggg agctaatttt aagcatgttc 3300
agtggcagct cccctccagt ttcagtgtca ctgttaaaat ttatcaaaaa gcaacttcac 3360
taggggtttt cttaagggat aaaggccttt tacagaagct aaaccttcc ccacatgtgg 3420
tagaatgtgc tcttctatat ctactcctca ataaagcatg ttctctgctc aaaaaaaaaa 3480
aaaaaaaaaa aaaaaaaaaa aaaa                                       3504
```

<210> 36
<211> 611
<212> PRT
<213> Homo sapiens

<220>
<223> HBO1 histone acetyltransferase, MYST histone acetyltransferase 2 (MYST2)

<400> 36

```
Met Pro Arg Arg Lys Arg Asn Ala Gly Ser Ser Ser Asp Gly Thr Glu
  1               5                  10                  15
```

```
Asp Ser Asp Phe Ser Thr Asp Leu Glu His Thr Asp Ser Ser Glu Ser
            20                  25                  30

Asp Gly Thr Ser Arg Arg Ser Ala Arg Val Thr Arg Ser Ser Ala Arg
        35                  40                  45

Leu Ser Gln Ser Ser Gln Asp Ser Ser Pro Val Arg Asn Leu Gln Ser
    50                  55                  60

Phe Gly Thr Glu Glu Pro Ala Tyr Ser Thr Arg Arg Val Thr Arg Ser
65                  70                  75                  80

Gln Gln Gln Pro Thr Pro Val Thr Pro Lys Lys Tyr Pro Leu Arg Gln
                85                  90                  95

Thr Arg Ser Ser Gly Ser Glu Thr Glu Gln Val Val Asp Phe Ser Asp
            100                 105                 110

Arg Glu Thr Lys Asn Thr Ala Asp His Asp Glu Ser Pro Pro Arg Thr
        115                 120                 125

Pro Thr Gly Asn Ala Pro Ser Ser Glu Ser Asp Ile Asp Ile Ser Ser
    130                 135                 140

Pro Asn Val Ser His Asp Glu Ser Ile Ala Lys Asp Met Ser Leu Lys
145                 150                 155                 160

Asp Ser Gly Ser Asp Leu Ser His Arg Pro Lys Arg Arg Arg Phe His
                165                 170                 175

Glu Ser Tyr Asn Phe Asn Met Lys Cys Pro Thr Pro Gly Cys Asn Ser
            180                 185                 190

Leu Gly His Leu Thr Gly Lys His Glu Arg His Phe Ser Ile Ser Gly
        195                 200                 205

Cys Pro Leu Tyr His Asn Leu Ser Ala Asp Glu Cys Lys Val Arg Ala
    210                 215                 220

Gln Ser Arg Asp Lys Gln Ile Glu Glu Arg Met Leu Ser His Arg Gln
225                 230                 235                 240

Asp Asp Asn Asn Arg His Ala Thr Arg His Gln Ala Pro Thr Glu Arg
                245                 250                 255

Gln Leu Arg Tyr Lys Glu Lys Val Ala Glu Leu Arg Lys Lys Arg Asn
            260                 265                 270

Ser Gly Leu Ser Lys Glu Gln Lys Glu Lys Tyr Met Glu His Arg Gln
        275                 280                 285

Thr Tyr Gly Asn Thr Arg Glu Pro Leu Leu Glu Asn Leu Thr Ser Glu
    290                 295                 300

Tyr Asp Leu Asp Leu Phe Arg Arg Ala Gln Ala Arg Ala Ser Glu Asp
305                 310                 315                 320

Leu Glu Lys Leu Arg Leu Gln Gly Gln Ile Thr Glu Gly Ser Asn Met
                325                 330                 335
```

```
Ile Lys Thr Ile Ala Phe Gly Arg Tyr Glu Leu Asp Thr Trp Tyr His
            340                 345                 350

Ser Pro Tyr Pro Glu Glu Tyr Ala Arg Leu Gly Arg Leu Tyr Met Cys
        355                 360                 365

Glu Phe Cys Leu Lys Tyr Met Lys Ser Gln Thr Ile Leu Arg Arg His
    370                 375                 380

Met Ala Lys Cys Val Trp Lys His Pro Pro Gly Asp Glu Ile Tyr Arg
385                 390                 395                 400

Lys Gly Ser Ile Ser Val Phe Glu Val Asp Gly Lys Lys Asn Lys Ile
                405                 410                 415

Tyr Cys Gln Asn Leu Cys Leu Leu Ala Lys Leu Phe Leu Asp His Lys
            420                 425                 430

Thr Leu Tyr Tyr Asp Val Glu Pro Phe Leu Phe Tyr Val Met Thr Glu
        435                 440                 445

Ala Asp Asn Thr Gly Cys His Leu Ile Gly Tyr Phe Ser Lys Glu Lys
    450                 455                 460

Asn Ser Phe Leu Asn Tyr Asn Val Ser Cys Ile Leu Thr Met Pro Gln
465                 470                 475                 480

Tyr Met Arg Gln Gly Tyr Gly Lys Met Leu Ile Asp Phe Ser Tyr Leu
                485                 490                 495

Leu Ser Lys Val Glu Glu Lys Val Gly Ser Pro Glu Arg Pro Leu Ser
            500                 505                 510

Asp Leu Gly Leu Ile Ser Tyr Arg Ser Tyr Trp Lys Glu Val Leu Leu
        515                 520                 525

Arg Tyr Leu His Asn Phe Gln Gly Lys Glu Ile Ser Ile Lys Glu Ile
    530                 535                 540

Ser Gln Glu Thr Ala Val Asn Pro Val Asp Ile Val Ser Thr Leu Gln
545                 550                 555                 560

Ala Leu Gln Met Leu Lys Tyr Trp Lys Gly Lys His Leu Val Leu Lys
                565                 570                 575

Arg Gln Asp Leu Ile Asp Glu Trp Ile Ala Lys Glu Ala Lys Arg Ser
            580                 585                 590

Asn Ser Asn Lys Thr Met Asp Pro Ser Cys Leu Lys Trp Thr Pro Pro
        595                 600                 605

Lys Gly Thr
    610
```

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CK2-specific siRNA molecule

<400> 37
aacattgaat tagatccacg t 21

<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PIM1-specific siRNA molecule

<400> 38
aaaactccga gtgaactggt c 21

<210> 39
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HBO1-specific siRNA molecule

<400> 39
aactgagcaa gtggttgatt t 21

<210> 40
<211> 409
<212> PRT
<213> Homo sapiens

<220>
<223> CDC7 cell division cycle 7 (CDC7), CDC7 cell division cycle 7-like 1 (CDC7L1) protein serine threonine kinase

<400> 40
Met Glu Ala Ser Leu Gly Ile Gln Met Asp Glu Pro Met Ala Phe Ser
1 5 10 15

Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu
20 25 30

Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr
35 40 45

Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile
50 55 60

Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln
65 70 75 80

```
Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile Pro Thr Ser
                  85                  90                  95

His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr Val Ala Gly
             100                 105                 110

Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg Lys Asn Asp
         115                 120                 125

His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser Phe Leu Asp
     130                 135                 140

Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr Met Leu Asn
145                 150                 155                 160

Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile Val His Arg
                165                 170                 175

Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu Lys Lys Tyr
             180                 185                 190

Ala Leu Val Asp Phe Gly Leu Ala Gln Gly Thr His Asp Thr Lys Ile
         195                 200                 205

Glu Leu Leu Lys Phe Val Gln Ser Glu Ala Gln Gln Glu Arg Cys Ser
     210                 215                 220

Gln Asn Lys Ser His Ile Ile Thr Gly Asn Lys Ile Pro Leu Ser Gly
225                 230                 235                 240

Pro Val Pro Lys Glu Leu Asp Gln Gln Ser Thr Thr Lys Ala Ser Val
                245                 250                 255

Lys Arg Pro Tyr Thr Asn Ala Gln Ile Gln Ile Lys Gln Gly Lys Asp
             260                 265                 270

Gly Lys Glu Gly Ser Val Gly Leu Ser Val Gln Arg Ser Val Phe Gly
         275                 280                 285

Glu Arg Asn Phe Asn Ile His Ser Ser Ile Ser His Glu Ser Pro Ala
     290                 295                 300

Val Lys Leu Met Lys Gln Ser Lys Thr Val Asp Val Leu Ser Arg Lys
305                 310                 315                 320

Leu Ala Thr Lys Lys Lys Ala Ile Ser Thr Lys Val Met Asn Ser Ala
                325                 330                 335

Val Met Arg Lys Thr Ala Ser Ser Cys Pro Ala Ser Leu Thr Cys Asp
             340                 345                 350

Cys Tyr Ala Thr Asp Lys Val Cys Ser Ile Cys Leu Ser Arg Arg Gln
         355                 360                 365

Gln Val Ala Pro Arg Ala Gly Thr Pro Gly Phe Arg Ala Pro Glu Val
     370                 375                 380
```

```
Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met Trp Ser Ala
385                 390                 395                 400

Gly Val Ile Phe Leu Ser Leu Leu Ser
                405
```

<210> 41
<211> 314
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<223> CDC7

<400> 41

```
Met Thr Ser Lys Thr Lys Asn Ile Asp Asp Ile Pro Pro Glu Ile Lys
  1               5                  10                  15

Glu Glu Met Ile Gln Leu Tyr His Asp Leu Pro Gly Ile Glu Asn Glu
             20                  25                  30

Tyr Lys Leu Ile Asp Lys Ile Gly Glu Gly Thr Phe Ser Ser Val Tyr
         35                  40                  45

Lys Ala Lys Asp Ile Thr Gly Lys Ile Thr Lys Lys Phe Ala Ser His
     50                  55                  60

Phe Trp Asn Tyr Gly Ser Asn Tyr Val Ala Leu Lys Lys Ile Tyr Val
 65                  70                  75                  80

Thr Ser Ser Pro Gln Arg Ile Tyr Asn Glu Leu Asn Leu Leu Tyr Ile
                 85                  90                  95

Met Thr Gly Ser Ser Arg Val Ala Pro Leu Cys Asp Ala Lys Arg Val
            100                 105                 110

Arg Asp Gln Val Ile Ala Val Leu Pro Tyr Tyr Pro His Glu Glu Phe
        115                 120                 125

Arg Thr Phe Tyr Arg Asp Leu Pro Ile Lys Gly Ile Lys Lys Tyr Ile
    130                 135                 140

Trp Glu Leu Leu Arg Ala Leu Lys Phe Val His Ser Lys Gly Ile Ile
145                 150                 155                 160

His Arg Asp Ile Lys Pro Thr Asn Phe Leu Phe Asn Leu Glu Leu Gly
                165                 170                 175

Arg Gly Val Leu Val Asp Phe Gly Leu Ala Glu Ala Gln Met Asp Tyr
            180                 185                 190

Lys Ser Met Ile Ser Ser Gln Asn Asp Tyr Asp Asn Tyr Ala Asn Thr
        195                 200                 205

Asn His Asp Gly Gly Tyr Ser Met Arg Asn His Glu Gln Phe Cys Pro
    210                 215                 220

Cys Ile Met Arg Asn Gln Tyr Ser Pro Asn Ser His Asn Gln Thr Pro
225                 230                 235                 240
```

```
Pro Met Val Thr Ile Gln Asn Gly Lys Val Val His Leu Asn Asn Val
                245                 250                 255

Asn Gly Val Asp Leu Thr Lys Gly Tyr Pro Lys Asn Glu Thr Arg Arg
            260                 265                 270

Ile Lys Arg Ala Asn Arg Ala Gly Thr Arg Gly Phe Arg Ala Pro Glu
        275                 280                 285

Val Leu Met Lys Cys Gly Ala Gln Ser Thr Lys Ile Asp Ile Trp Ser
    290                 295                 300

Val Gly Val Ile Leu Leu Ser Leu Leu Gly
305                 310


<210> 42
<211> 294
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:protein kinase
      consensus sequence

<400> 42
Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
  1               5                  10                  15

Lys Ala Lys His Lys Asp Lys Thr Gly Lys Ile Val Ala Val Lys Ile
             20                  25                  30

Leu Lys Lys Glu Lys Glu Ser Ile Lys Glu Lys Arg Phe Leu Arg Glu
         35                  40                  45

Ile Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Ile
     50                  55                  60

Gly Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr
 65                  70                  75                  80

Met Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Gly Pro
                85                  90                  95

Leu Ser Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly
            100                 105                 110

Leu Glu Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro
        115                 120                 125

Glu Asn Ile Leu Leu Asp Glu Asn Asp Gly Thr Val Lys Ile Ala Asp
    130                 135                 140

Phe Gly Leu Ala Arg Leu Leu Glu Ser Ser Ser Lys Leu Thr Thr Phe
145                 150                 155                 160

Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile Leu Glu Gly
                165                 170                 175

Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly Val Ile Leu
            180                 185                 190
```

```
Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro
        195                 200                 205

Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile Phe Val Leu
    210                 215                 220

Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile Asp Pro Leu
225                 230                 235                 240

Glu Glu Leu Phe Arg Ile Ile Lys Arg Pro Gly Leu Arg Leu Pro Leu
                245                 250                 255

Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
            260                 265                 270

Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
        275                 280                 285

Leu Asn His Pro Trp Phe
    290
```

<210> 43
<211> 253
<212> PRT
<213> Homo sapiens

<220>
<223> cytokine-inducible kinase (CNK) serine threonine kinase, proliferation-related kinase (PRK), polo-like kinase 3 (PLK3)

<400> 43

```
Tyr Leu Lys Gly Arg Leu Leu Gly Lys Gly Gly Phe Ala Arg Cys Tyr
  1               5                  10                  15

Glu Ala Thr Asp Thr Glu Thr Gly Ser Ala Tyr Ala Val Lys Val Ile
             20                  25                  30

Pro Gln Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Leu Asn
         35                  40                  45

Glu Ile Glu Leu His Arg Asp Leu Gln His Arg His Ile Val Arg Phe
     50                  55                  60

Ser His His Phe Glu Asp Ala Asp Asn Ile Tyr Ile Phe Leu Glu Leu
 65                  70                  75                  80

Cys Ser Arg Lys Ser Leu Ala His Ile Trp Lys Ala Arg His Thr Leu
                85                  90                  95

Leu Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Leu Ser Gly Leu
            100                 105                 110

Lys Tyr Leu His Gln Arg Gly Ile Leu His Arg Asp Leu Lys Leu Gly
        115                 120                 125

Asn Phe Phe Ile Thr Glu Asn Met Glu Leu Lys Val Gly Asp Phe Gly
    130                 135                 140
```

```
Leu Ala Ala Arg Leu Glu Pro Pro Glu Gln Arg Lys Lys Thr Ile Cys
145                 150                 155                 160

Gly Thr Pro Asn Tyr Val Ala Pro Glu Val Leu Leu Arg Gln Gly His
                165                 170                 175

Gly Pro Glu Ala Asp Val Trp Ser Leu Gly Cys Val Met Tyr Thr Leu
            180                 185                 190

Leu Cys Gly Ser Pro Pro Phe Glu Thr Ala Asp Leu Lys Glu Thr Tyr
        195                 200                 205

Arg Cys Ile Lys Gln Val His Tyr Thr Leu Pro Ala Ser Leu Ser Leu
    210                 215                 220

Pro Ala Arg Gln Leu Leu Ala Ala Ile Leu Arg Ala Ser Pro Arg Asp
225                 230                 235                 240

Arg Pro Ser Ile Asp Gln Ile Leu Arg His Asp Phe Phe
                245                 250
```

<210> 44
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 44
```
His Arg Asp Leu Lys
  1               5
```

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 45
```
Asp Phe Gly Leu Ala
  1               5
```

<210> 46
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 46
Ala Pro Glu Val
1

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 47
Asp Val Trp Ser Leu Gly
1 5

<210> 48
<211> 256
<212> PRT
<213> Homo sapiens

<220>
<223> serine threonine kinase 2 (STK2, NEK4)

<400> 48
Tyr Cys Tyr Leu Arg Val Val Gly Lys Gly Ser Tyr Gly Glu Val Thr
1 5 10 15

Leu Val Lys His Arg Arg Asp Gly Lys Gln Tyr Val Ile Lys Lys Leu
20 25 30

Asn Leu Arg Asn Ala Ser Ser Arg Glu Arg Arg Ala Ala Glu Gln Glu
35 40 45

Ala Gln Leu Leu Ser Gln Leu Lys His Pro Asn Ile Val Thr Tyr Lys
50 55 60

Glu Ser Trp Glu Gly Gly Asp Gly Leu Leu Tyr Ile Val Met Gly Phe
65 70 75 80

Cys Glu Gly Gly Asp Leu Tyr Arg Lys Leu Lys Glu Gln Lys Gly Gln
85 90 95

Leu Leu Pro Glu Asn Gln Val Val Glu Trp Phe Val Gln Ile Ala Met
100 105 110

Ala Leu Gln Tyr Leu His Glu Lys His Ile Leu His Arg Asp Leu Lys
115 120 125

Thr Gln Asn Val Phe Leu Thr Arg Thr Asn Ile Ile Lys Val Gly Asp
130 135 140

Leu Gly Ile Ala Arg Val Leu Glu Asn His Cys Asp Met Ala Ser Thr
145 150 155 160

Leu Ile Gly Thr Pro Tyr Tyr Met Ser Pro Glu Leu Phe Ser Asn Lys
165 170 175

```
Pro Tyr Asn Tyr Lys Ser Asp Val Trp Ala Leu Gly Cys Cys Val Tyr
            180                 185                 190

Glu Met Ala Thr Leu Lys His Ala Phe Asn Ala Lys Asp Met Asn Ser
        195                 200                 205

Leu Val Tyr Arg Ile Ile Glu Gly Lys Leu Pro Pro Met Pro Arg Asp
    210                 215                 220

Tyr Ser Pro Glu Leu Ala Glu Leu Ile Arg Thr Met Leu Ser Lys Arg
225                 230                 235                 240

Pro Glu Glu Arg Pro Ser Val Arg Ser Ile Leu Arg Gln Pro Tyr Ile
                245                 250                 255


<210> 49
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 49
His Pro Asn Ile Val
  1               5


<210> 50
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 50
Glu Gly Gly Asp Leu
  1               5


<210> 51
<211> 294
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:protein kinase
      consensus sequence

<400> 51
Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
  1               5                  10                  15

Lys Ala Lys His Lys Asp Lys Thr Gly Lys Ile Val Ala Val Lys Ile
            20                  25                  30
```

```
Leu Lys Lys Glu Lys Glu Ser Ile Lys Glu Lys Arg Phe Leu Arg Glu
          35                  40                  45

Ile Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Ile
     50                  55                  60

Gly Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr
 65                  70                  75                  80

Met Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Gly Pro
                 85                  90                  95

Leu Ser Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly
            100                 105                 110

Leu Glu Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro
        115                 120                 125

Glu Asn Ile Leu Leu Asp Glu Asn Asp Gly Thr Val Lys Ile Ala Asp
    130                 135                 140

Phe Gly Leu Ala Arg Leu Leu Glu Ser Ser Ser Lys Leu Thr Thr Phe
145                 150                 155                 160

Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile Leu Glu Gly
                165                 170                 175

Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly Val Ile Leu
            180                 185                 190

Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro
        195                 200                 205

Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile Phe Val Leu
    210                 215                 220

Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile Asp Pro Leu
225                 230                 235                 240

Glu Glu Leu Phe Arg Ile Ile Lys Arg Pro Gly Leu Arg Leu Pro Leu
                245                 250                 255

Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
            260                 265                 270

Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
        275                 280                 285

Leu Asn His Pro Trp Phe
    290
```

<210> 52
<211> 286
<212> PRT
<213> Homo sapiens

<220>
<223> serine threonine protein kinase casein kinase 2, alpha 1 subunit isoform a, transcript variant 2 (CK2, CK2alpha), CK2 catalytic subunit alpha

<400> 52
Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly Lys Tyr Ser Glu Val Phe
1 5 10 15

Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys Val Val Val Lys Ile Leu
20 25 30

Lys Pro Val Lys Lys Lys Lys Ile Lys Arg Glu Ile Lys Ile Leu Glu
35 40 45

Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr Leu Ala Asp Ile Val Lys
50 55 60

Asp Pro Val Ser Arg Thr Pro Ala Leu Val Phe Glu His Val Asn Asn
65 70 75 80

Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu Thr Asp Tyr Asp Ile Arg
85 90 95

Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu Asp Tyr Cys His Ser Met
100 105 110

Gly Ile Met His Arg Asp Val Lys Pro His Asn Val Met Ile Asp His
115 120 125

Glu His Arg Lys Leu Arg Leu Ile Asp Trp Gly Leu Ala Glu Phe Tyr
130 135 140

His Pro Gly Gln Glu Tyr Asn Val Arg Val Ala Ser Arg Tyr Phe Lys
145 150 155 160

Gly Pro Glu Leu Leu Val Asp Tyr Gln Met Tyr Asp Tyr Ser Leu Asp
165 170 175

Met Trp Ser Leu Gly Cys Met Leu Ala Ser Met Ile Phe Arg Lys Glu
180 185 190

Pro Phe Phe His Gly His Asp Asn Tyr Asp Gln Leu Val Arg Ile Ala
195 200 205

Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp Tyr Ile Asp Lys Tyr Asn
210 215 220

Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile Leu Gly Arg His Ser Arg
225 230 235 240

Lys Arg Trp Glu Arg Phe Val His Ser Glu Asn Gln His Leu Val Ser
245 250 255

Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu Leu Arg Tyr Asp His Gln
260 265 270

Ser Arg Leu Thr Ala Arg Glu Ala Met Glu His Pro Tyr Phe
275 280 285

<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 53
Val Lys Ile Leu Lys
1 5

<210> 54
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 54
Trp Ser Leu Gly
1

<210> 55
<211> 298
<212> PRT
<213> Homo sapiens

<220>
<223> cyclin-dependent kinase 2 (CDK2)

<400> 55
Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
1 5 10 15

Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu
20 25 30

Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala
35 40 45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val
50 55 60

Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe
65 70 75 80

Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu
85 90 95

Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
100 105 110

Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu
115 120 125

Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala
130 135 140

Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr
145 150 155 160

```
His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly
                165                 170                 175

Cys Lys Tyr Tyr Ser Thr Ala Val Asp Ile Trp Ser Leu Gly Cys Ile
            180                 185                 190

Phe Ala Glu Met Val Thr Arg Arg Ala Leu Phe Pro Gly Asp Ser Glu
        195                 200                 205

Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr Leu Gly Thr Pro Asp Glu
    210                 215                 220

Val Val Trp Pro Gly Val Thr Ser Met Pro Asp Tyr Lys Pro Ser Phe
225                 230                 235                 240

Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys Val Val Pro Pro Leu Asp
                245                 250                 255

Glu Asp Gly Arg Ser Leu Leu Ser Gln Met Leu His Tyr Asp Pro Asn
            260                 265                 270

Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala His Pro Phe Phe Gln Asp
        275                 280                 285

Val Thr Lys Pro Val Pro His Leu Arg Leu
    290                 295
```

<210> 56
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Xeroderma pigmentosum complementation group XPG N-terminal domain (XPG_N) consensus sequence

<400> 56

```
Met Gly Ile Lys Gly Leu Leu Pro Ile Leu Lys Pro Val Ala Pro Glu
  1               5                  10                  15

Ala Ile Arg Ser Val Ser Ile Glu Ala Leu Glu Gly Tyr Tyr Lys Val
             20                  25                  30

Leu Ala Ile Asp Ala Ser Ile Trp Leu Tyr Gln Phe Leu Lys Ala Val
         35                  40                  45

Arg Asp Gln Leu Gly Asn Asn Leu Glu Asn Glu Glu Gly Glu Thr Thr
     50                  55                  60

Ser His Leu Met Gly Leu Phe Ser Arg Leu Cys Arg Leu Leu Asp Phe
 65                  70                  75                  80

Gly Ile Lys Pro Ile Phe Val Phe Asp Gly Gly Ala Pro Asn Asp Leu
                 85                  90                  95

Lys Ala Glu Thr Leu Gln Lys Arg Ser Ala Arg Arg Gln Glu Ala
            100                 105                 110
```

<210> 57
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> flap structure-specific endonuclease 1 (FEN1)
5'-3' exonuclease

<400> 57
Met Gly Ile Gln Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser
1 5 10 15

Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
20 25 30

Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
35 40 45

Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
50 55 60

Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
65 70 75 80

Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
85 90 95

Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala
100 105

<210> 58
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 58
Ala Ile Asp Ala Ser
1 5

<210> 59
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 59
Tyr Gln Phe Leu
1

<210> 60
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 60
Asn Glu Glu Gly Glu Thr Thr Ser His Leu Met Gly
1 5 10

<210> 61
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 61
Gly Ile Lys Pro
1

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 62
Val Phe Asp Gly
1

<210> 63
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Xeroderma
pigmentosum complementation group XPG I-region
domain (XPG_I) consensus sequence

<400> 63
Arg Leu Met Gly Ile Pro Tyr Ile Val Ala Pro Gly Val Glu Ala Glu
1 5 10 15

Ala Gln Cys Ala Tyr Leu Glu Lys Lys Gly Leu Val Asp Gly Ile Ile
20 25 30

Thr Glu Asp Ser Asp Val Leu Leu Phe Gly Ala Pro Arg Leu Leu Arg
35 40 45

```
Asn Leu Thr Leu Ser Gly Lys Lys Ser Gly Pro Ser Ile Thr Ser Leu
     50                  55                  60

Lys Val Glu Ile Glu Glu Ile Asp Leu Glu Ser Leu Leu Arg Glu Leu
 65                  70                  75                  80

Gly Leu Gly Lys Leu Ser Arg Glu Gln Leu Ile Asp Leu Ala Ile Leu
                 85                  90                  95

Leu Gly Cys Asp Tyr Thr Glu Gly
            100


<210> 64
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<223> flap structure-specific endonuclease 1 (FEN1)
      5'-3' exonuclease

<400> 64
Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu Ala
  1               5                  10                  15

Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala Thr
             20                  25                  30

Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg His
         35                  40                  45

Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu
     50                  55                  60

Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp
 65                  70                  75                  80

Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser
                 85                  90


<210> 65
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 65
Leu Met Gly Ile Pro Tyr
  1               5


<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 66
Glu Ala Glu Ala
1

<210> 67
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 67
Glu Leu Gly Leu
1

<210> 68
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 68
Ile Leu Leu Gly
1

<210> 69
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<223> HBO1 histone acetyltransferase, MYST histone
acetyltransferase 2 (MYST2)

<400> 69
Tyr His Ser Pro Tyr Pro Glu Glu Tyr Ala Arg Leu Gly Arg Leu Tyr
1 5 10 15

Met Cys Glu Phe Cys Leu Lys Tyr Met Lys Ser Gln Thr Ile Leu Arg
20 25 30

Arg His Met Ala Lys Cys Val Trp Lys His Pro Pro Gly Asp Glu Ile
35 40 45

Tyr Arg Lys Gly Ser Ile Ser Val Phe Glu Val Asp Gly Lys Lys Asn
50 55 60

Lys Ile Tyr Cys Gln Asn Leu Cys Leu Leu Ala Lys Leu Phe Leu Asp
65 70 75 80

```
His Lys Thr Leu Tyr Tyr Asp Val Glu Pro Phe Leu Phe Tyr Val Met
                 85                  90                  95

Thr Glu Ala Asp Asn Thr Gly Cys His Leu Ile Gly Tyr Phe Ser Lys
            100                 105                 110

Glu Lys Asn Ser Phe Leu Asn Tyr Asn Val Ser Cys Ile Leu Thr Met
        115                 120                 125

Pro Gln Tyr Met Arg Gln Gly Tyr Gly Lys Met Leu Ile Asp Phe Ser
    130                 135                 140

Tyr Leu Leu Ser Lys Val Glu Glu Lys Val Gly Ser Pro Glu Arg Pro
145                 150                 155                 160

Leu Ser Asp Leu Gly Leu Ile Ser Tyr Arg Ser Tyr Trp Lys Glu Val
                165                 170                 175

Leu Leu Arg Tyr Leu His Asn Phe Gln Gly Lys Glu Ile Ser Ile Lys
            180                 185                 190

Glu Ile Ser Gln Glu Thr Ala Val Asn Pro Val Asp Ile Val Ser Thr
        195                 200                 205

Leu Gln Ala Leu Gln Met Leu Lys Tyr Trp Lys Gly Lys His Leu Val
    210                 215                 220

Leu Lys Arg Gln Asp Leu Ile Asp Glu Trp Ile Ala Lys Glu Ala Lys
225                 230                 235                 240

Arg Ser Asn Ser Asn Lys Thr Met Asp Pro Ser Cys Leu Lys Trp Thr
                245                 250                 255

Pro Pro Lys Gly Thr
            260
```

<210> 70
<211> 265
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<223> Esa1

<400> 70

```
Tyr Phe Ser Pro Tyr Pro Ile Glu Leu Thr Asp Glu Asp Phe Ile Tyr
  1               5                  10                  15

Ile Asp Asp Phe Thr Leu Gln Tyr Phe Gly Ser Lys Lys Gln Tyr Glu
             20                  25                  30

Arg Tyr Arg Lys Lys Cys Thr Leu Arg His Pro Pro Gly Asn Glu Ile
         35                  40                  45

Tyr Arg Asp Asp Tyr Val Ser Phe Phe Glu Ile Asp Gly Arg Lys Gln
     50                  55                  60

Arg Thr Trp Cys Arg Asn Leu Cys Leu Leu Ser Lys Leu Phe Leu Asp
 65                  70                  75                  80
```

```
His Lys Thr Leu Tyr Tyr Asp Val Asp Pro Phe Leu Phe Tyr Cys Met
                 85                  90                  95

Thr Arg Arg Asp Glu Leu Gly His His Leu Val Gly Tyr Phe Ser Lys
            100                 105                 110

Glu Lys Glu Ser Ala Asp Gly Tyr Asn Val Ala Cys Ile Leu Thr Leu
        115                 120                 125

Pro Gln Tyr Gln Arg Met Gly Tyr Gly Lys Leu Leu Ile Glu Phe Ser
    130                 135                 140

Tyr Glu Leu Ser Lys Lys Glu Asn Lys Val Gly Ser Pro Glu Lys Pro
145                 150                 155                 160

Leu Ser Asp Leu Gly Leu Leu Ser Tyr Arg Ala Tyr Trp Ser Asp Thr
                165                 170                 175

Leu Ile Thr Leu Leu Val Glu His Gln Lys Glu Ile Thr Ile Asp Glu
            180                 185                 190

Ile Ser Ser Met Thr Ser Met Thr Thr Thr Asp Ile Leu His Thr Ala
        195                 200                 205

Lys Thr Leu Asn Ile Leu Arg Tyr Tyr Lys Gly Gln His Ile Ile Phe
    210                 215                 220

Leu Asn Glu Asp Ile Leu Asp Arg Tyr Asn Arg Leu Lys Ala Lys Lys
225                 230                 235                 240

Arg Arg Thr Ile Asp Pro Asn Arg Leu Ile Trp Lys Pro Pro Val Phe
                245                 250                 255

Thr Ala Ser Gln Leu Arg Phe Ala Trp
            260                 265
```

<210> 71
<211> 253
<212> PRT
<213> Homo sapiens

<220>
<223> PIM1 oncogene serine threonine kinase

<400> 71

```
Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser Val Tyr
  1               5                  10                  15

Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val Ala Ile Lys His Val
             20                  25                  30

Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu Pro Asn Gly Thr Arg
         35                  40                  45

Val Pro Met Glu Val Val Leu Leu Lys Lys Val Ser Ser Gly Phe Ser
     50                  55                  60

Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg Pro Asp Ser Phe Val
 65                  70                  75                  80
```

```
Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp Leu Phe Asp Phe Ile
                85                  90                  95

Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala Arg Ser Phe Phe Trp
            100                 105                 110

Gln Val Leu Glu Ala Val Arg His Cys His Asn Cys Gly Val Leu His
        115                 120                 125

Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Asn Arg Gly Glu
    130                 135                 140

Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val
145                 150                 155                 160

Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile
                165                 170                 175

Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala Val Trp Ser Leu Gly
            180                 185                 190

Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu His Asp
        195                 200                 205

Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg Gln Arg Val Ser Ser
    210                 215                 220

Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp
225                 230                 235                 240

Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro Trp Met
                245                 250
```

<210> 72
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 72
Asp Leu Phe Asp
1

<210> 73
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 73
Glu Asn Ile Leu
1

<210> 74
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 74
Val Trp Ser Leu Gly
1 5

<210> 75
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 75
Asn His Pro Trp
1

<210> 76
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:5'-end
32P-labeled oligonucleotide primer

<400> 76
cactgactgt atg 13

<210> 77
<211> 30
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA
Molecule:oligonucleotide template

<220>
<223> Description of Artificial Sequence:oligonucleotide
template

<400> 77
ctcgtcagca tcttcaucat acagtcagtg 30

<210> 78
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly Gly
flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present
or absent

<400> 78
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
35 40 45

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
50 55 60

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65 70 75 80

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
85 90 95

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
100 105 110

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
115 120 125

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
130 135 140

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
145 150 155 160

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
165 170 175

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
180 185 190

Gly Gly Gly Gly Gly Gly Gly Gly
195 200